

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGTGCAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCCTCAGGAGGTGCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCGTCCGGGGGATGACTGATTCTCCTCCGCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGTGTATGTGGCT
TCTGTGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCCGCTAC
CGCCGACGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAG
GACCAAGCGGCTTCTTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGTTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGAGGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAAGTCAGAGGCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGTGGGGTCTGTCTCCTGCAAGAAAAGACTCGTGACTGCCAGCGCCCCAGG
CTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTTCTCTCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCTTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTTGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCTGACCCCCAGCACAAATAAAATGAAA
CGTGAAAGGGCGGCCGCACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGTT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPPCRNGGSCVQPGRRCRCPAGWRGDTCCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCPVKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCCCAGCGCGGGACTATGTTGAAATTCGCGCGCTCAGCAGCTACTGGCCCCGTGATC
CGGTTCTTGGTGCCCTGGGCATCAACACATAGCCATCGACTTCGGGGAGCAGGCCCTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATCGAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTTCACGGGTCCATGAGTGACTTCAAAAATGTGGGCGCTGTGTGTT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC
TCCCGTCTTTTACACACATGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATTGTGGACGAGTCGGTGGGAGCAAGACGAGAAGGGCCTTCTGTACTCTCGCGCCCTTT
CCTTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
CCTGGTGGGATGTGCCCTCAATCTCAGATGTCATAGCTCAGGTGTGTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGAGCCCCGTCTCATCCCCGATCCTCTCCTGTACATGGGC
GCATTTGTGCGCTGCACCACCTTGTGCCCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATCGTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACTTGTGTGGCAGTTCTGCGACCAACAGAGCAGTGGCGCAATTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCTGCTTTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC
AAGAAGTTCACCTTCTGCTGTCATGGCTCTGTCACTCAGCTCTGTGTTTCGTGATGTTTTGGAC
ACCCAACTGCTTGTAGAAAACTTTGATAGACATCATCGGATGGACTTGGCCTTTGCAGAAC
TCTGTGTTGTTCTTTTGGCGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACGGGTGGCTGATGACATGAAGAAAACTTCTGCTTGTGCCCCAGCTCTGTGCTGCG
GATCATCGTCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGGGACCC
TGGGCGTGGGCTCCCTCTGGCGGGCTTTGTGGGAGAAATCCACCATGGTGCGCATCGCTGCG
TGCTATGTCATCCGGAACGAGAAAAAGAGATGGAGAATGAGTCGGCCACGAGGGGGGAAGA
CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAAGGCACGGGACGCCATGGGCAGTGCAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTCTCCCTTTTTTGTGTTTGTGTTGTAAT
GAAAGAGGCGCTGATTTAAAGTTTCTGTGTCATTTCTTAGCATATCGGGTATGCTCACACT
GACGGGGGACCTAGTGAATGCTTTTACTGTTGTATGTAATAAACAACAAACAACTGAC
TTCATACCCCTGCCTCACGAAAAACCAAAGACACAGCTGCCTCAGGTTGACGTTGTGTCC
TCTTCCCTTGGACAATCTCTCTTGGAAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCTTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
TAAAACTCGGCTTCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTTGAACCACTTACTCCACACATGCAG
GAGGGGGGTGGCACGCTGCAGCCCGAGTCCCCGTTGCACATGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCCGGG
GGCAGCAAACTGACATGTTGTAATGATAGCAATTCACTCTGCGTTCTCCTAGATCTGAGCAA
GCTGTGCTGCTTCTACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTTGTCAAAAA
GCGCATCTCCAGATTTCCAGACCTTCCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
CTTTCTGAAGGTCGATTAGAGCGAGTCACATGGAGCATCTTAACCTTTGCAATTTAGTTT
TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGATGTACTACGGTATCTCCCTCCACACATACAGATAAAGCAAGACATTTTATAACG
ATACAGAGTCACTATGTGGTCTCCTCCCTGAAATAACGCATTCGAATTCATGAGTGCAGTA
TATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAAATATAGACACGTTTCACT
AAATTTGATTTAGTCAGAAATCTTAGACTGAAAGAACCTAAACAAAAAAATTTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTATTTTTCG
ATTTTCAATAAAATGCTCTAATAACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIINKLHHVDES
GSKTRRAFLYLAAFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLILIPILSLYMGALVRCTTTLCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelCVVPLR
IFSFFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRRIIVLIASLVVLPYLGVBHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
 GCCNTTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCGAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
 CCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCGTCTTTCG
 ACAAGAATAACCCCGAGCAAAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
 AAGAAGTTTCAACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
 ACCCAACGTGCTCGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
 TCTGTGTTGTTCTCTGCGGATCTTCTCTCTTCCAGTTCAGTACAGTGAAGGGCGCAT
 CTCACCGGTGCTGTATGCAGCTGAAGAAAAACCTTCGTG

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCITTTGCGGATTTTCT
CCTTTTCCAGTTCAGTCACAGNGAGGGCGCATCTCACCGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCTCCTGCGGGGCA

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FIGURE 7

TATTCCCAGTTCGGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGAACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

FIGURE 8

GCCCCGCGCCCGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGCGGGGCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGGCTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAATCCACCGTGAGCCGCTCATCTTACAGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATATGCTGAGCCCGGGCGTGAGAGTCACTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTCTCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTCACCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGCTCGTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCTTGAACACAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCATTCGCGTGCCTGGTACGCAGGCCCTTCTTCTTCACTCTCCTCTT
CTACTTGTGTGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTTGCCCAAGGTCCAGGACGCCAGCCCACTCGGGTCTGTGTCAGGCCCTCGGTCT
CACCCCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTTGTGGGCCTCATCATCTTCTCTGTGCAACCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGCCGGGGCC
TTTGACAACGAGCAGGACGGCGTCACTTACAGCTACTCCTTCTTCCACTTCTGCTGTGTCT
GGCCTCACTGCACGTCTGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCAGCTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCTTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCGAGCTCCAGGACCTG
CCCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTTCTTCTTCCCCCTCCTCCTGT
TGCCCCATCTCAGCATCTCGGATGAAAGGGCTCCTTGTCTCTCAGGCTCCACGGGAGCGGG
CTGCTGGAGAGAGCGGGGAACCTCCACACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCAAGTCCCCCAGGGGACCTGCCCTTCTTGGACTTCTGTGCTTACTGAGTCTCT
AAGACTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

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FIGURE 9

MGACLGACSLSCASCILCGSAPCILSCCCPASRNSTVSRIFTFFFLGLVLSIIMLSPGVE
SQLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLILQLVLLIDFAHSW
NQRWLKAEEDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHGKVFISLNLTF
VCVSIAAVLKPVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTECPMLDATQQQQQVA
ACEGRAFDNEQDGVITYSYSFFHFCVLVSLHVMMLTNWYKPGETRMISTWTAVVVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

GAGCGAGGCCGGGGAC TGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTAGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCTTGAGCGCTCAAGTTTGTCCGTAGGTCTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCGCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTCCGGAAGTCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATAACACGCTTTTATCATGCTAAACAACAATACATGTAGCAGAGCCAGGCA
GAAATTTATCATAACCCGTTGAGTGTGTGCAATCTGCAATCGTGTGCCACAGGAGCTT
CAATTCGTTATGGCTGGCGCTGGGTTTGGAGAATCTGAGTGTTTGTGACTATATTCAACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATGCGAGA
GCTGTACCGGGAAGTCTTTTTAGGATAAACGTAGGCCTCGCTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTCAGGAAAGAAAAAGAAAGGATCGAAAGGCATCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAAATGATGCTAAGAAAAATTGAAGCACTGCTAAACCTTCTTAGAAACC
CTTCAGTAATAGATAAACAAAGACAAGGACTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTCTTTTCTTTTCTT
TTTAACTAAGTAAGGGGCTGTTGTACTCTCATTCTTACTTATCTTAAATTTAAATACATACT
TATGTTTGTATTAACTATCAATATGCTGATACATGCGATATCAACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTCCGAAAAGATTAAAGTTGAATTTTACAGTTT

Important Features:

amino acids 1-24

amino acids 76-96 and 171-195

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCCGCCGCCGCCGCCGCCGCCGCTGCAGCCCCAGGCCCCGGCCCCCACCACGCTCT
GCGTTGCTGCCCGCCCTGGGCCAGGCCCCAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGCTTTCGCGGG
GCTTCGCGTGTTCGAAGAACGCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAAATGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCAATGCACTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTATT
GTTCAGTTTTCTGTATCTTTCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTCCGAAGTGTTAAACCATAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCGCGCAATCCTAGTGCATTCCTTTGATGAGAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTGTTCACTTTCTGTAATTTCTGTGTTAAGCTCCATTGCCCAGT
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATGATAGTGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTTCTTTCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTTCATTGTGCGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTTAACTGCAGAAAACTTTGTATGTTACCACTGTGTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
TGGAAAAAGAGTGGAAATTTATTAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATCCCCAATTTTTTTTGGTCTTTTTTAGGAAAGATGTTGTGGTAAAAAGTGTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATGTGGTTTAAATTTTGACTTTTACAGGTAAAGTGCAAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTAAACAAGTTAGTATTAAATGCGTTGGCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCCAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAGGACAGAAACCTTCTTGTGTATGATGTTTGA
ATTAAGGAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLVFIVQFSVSCACALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

097609 101601

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTTATTGTTTCAGTTTTINTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTGTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCG

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FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTAGGGAAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATCTAGAATAG
TTATGTCTTAGGAAATGTGGTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATGTGTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

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FIGURE 18

ATGATTATTCTGTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTAAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCA~~C~~CA~~T~~GAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTCACTGAACCCCTCCACCTGATTTGTGTCTTATGACTGGCTG
ATCTCCAAAGGTCCAGCCAGCCAGTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAGGCAGACAGCGGGCACTACCAC
TGCACTGGCATCTTCCAGAGCCCTGGTCTTGGGATCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGA~~A~~CTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTCGAGAGGTCAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTTCAGAAGATCACTCCGGGTCACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACTGAATCCAGCTCCTCAGAAATCAGCTGTCTCCAGGAACCTGCTCCTGA
GGAGGCCCCCTGGGCCTTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATGAAGTAACAGTTCATCCATGATCTCACT
TAACCA~~C~~CCCAATAAAATCTGATTCTTTATTTCTCTTCTGCTGCAATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTGTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT
ATATAAAGTGAGAAATTAGAGTTTAGCTATAATTTGTGTTATCTCTTAAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAAATGTTGTGATTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGCAATTTTGC~~C~~CCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACAACGAA~~A~~ATAATCTGGCCCAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCAGCCTCATTAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTCTTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATT~~T~~AAAAAGGCCCCAGAGAGCTAACTACCCCTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCCCAACACCG
ACTCTGTCTGTGCTTGTATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAATTTCTGG
TTGTTTGTAGCCTAA

09978298-101501

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPFVFEGLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

00073238 101401

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGCGGTCCGCCACGCGTCCGGGCCACAGAAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAAGTAGCTCTGGCTGTGATGGGG
ATCTTA CTGGGCTGTACTCTCTGGGGCACCTAACAGTGGACCTTATGGCCGTCCCATCCT
GGAAGTGCAGAGAGTGTACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCT
GTCAACATCTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAAGTACCAGGGCCG
CCTGCATGTAGCCACAAGGTTCCAGGAGATGTATCCTCCCAATTGAGCACCCTGGAGATGG
ATGACCGGAGCCACTACAGCTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTACAGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACAGGAAACCATC
AAAGTAGCAACCTAAGTACCTTACTCTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCACTGTCTGGGCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCAGAGACC
AATCCTAAGGCCGAGGCGCTTCAAGGTGAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCTGATAATTAATTGGCAAGAAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAAACCATGAGGGTGGCCATCTTCGAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATGCCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAAATGCCCATTAGGC
CAGGATCTGCTGACATAATTGCTAGTCAGTCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTCTCGGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAAGGCCAGACAGCTTTTAAATTGAAATTGTTATTTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRFILEVPESVTGPGWKGDVNLPCTYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQAKYQGRHLHVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTDTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

00078203-101501

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGGTGCAGCCACCTCGCGGCACCCCGAGGCGCGCGCCAGCTCGCCGAGGTCCGTCCGA
 GCGCCCGGGCCCGCCCGGAGCCAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGGATGTCCCTCCTCTCTCTCTGCTAGTTTCCTACTATGTTGGAACCTTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGGCCCTGCCACCATCAACTGGGGC
 TTCAGAAAAAGCACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGAACCAAAA
 GTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATACTTGAAGTGGAGAACAGAAAGGGCCG
 AGTGGCCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCCTCTTGAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCCCTGGACGAGTTCTGCTGCAGAATCTTACCATTGCTACTCTGGACTGTA
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTCCGAGTAACCTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTTCGAGAAGATGCTGAAGCTCCAAAGGCCGTCTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTCTTCTCTCCACTCGCTCCACAGCAAAT
 AGTGCCCTCAGCGAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGCTCTGAATTACAATGGACTTGACTCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTTGGAGCTCAAGTCACAGCCACACAACAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCAAGGAACAGATTGAGATGAGCATTTCCTTATACAATACCAAAACAGCAAA
 AGGATGTAAGCTGATTCATCTGTAATAAGGCATCTTATTGTGCCCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTTGACAGGACCTGTGGTGAGAAAGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGATCAGTGCTTTGATTCACAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCAATTTCTGCAAACTTATTGGATT
 ATTAGTTATTTCAGACAGTCAAGCAGAACCACAGCCCTATTACACTGCTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTATAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAATAAC
 TATGAAAGGAGACAAAATTTGTGCAAAAGGATTGTGAAGAGCTTTCATCTTCTATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCAAAT
 CAGATCCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACTATGTCATT
 TATCAACGTCCTTAGAAAGTAATTTCTCTAGAGAAAAGGGATCTAGAAATGCTGAAAGATT
 CCAACATACCACTTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAAGAAATTGCAAGA
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGAGTGAGCCGAGATTATGCC
 ATTGCACTCAGCCTGGGTGACAGAGCGGGACTCCGCTCTC

097329.101501

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

00073233 101501
10510 9233420

FIGURE 25

GTGCTTCCTTGTCTCTCGCGCCAGTCTCTCTCCCTGGTTCTCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
 GAGCGGGGCTGCACTCGCGGGGCTTCTCCCGCTCGGGCGGCTGCGCTGGGCGAGTGCTGAGCGGCCCTTAG
 AGCCCTCCCTTGGCGCTCTCCCTCTCTCGCGGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCGGAGGCGCGGCTGGATGCGGCGCTGGGCGAGAAGCAGCGCGGATTTCAGCTGTCCCGCGCGCGCGGGCG
 CCCCTGCGAGTCCCGGTTTCAGCCATGGGGAACCTTCTCCGAGCAGCAGCACCGCCCTGCGCTCTCGACCGCATC
 GCCCGCGAGCCACAGCAAGATGATCGCGGCTCCCTTCTCTGCTTGGATTCTCTAGACACCAACACAGCTCAG
 CCAGAACAGGAAGCCCTGGAATCTCATTTGACACATACCGCATGTGTGACCGTGCACCGGCGAGGTGTCTAACCTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAGCGCTGCGCTCTGACGCAATGTCCCT
 GTGGGACCTTTACAGGACATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCTCCATGGCCAAATG
 ATTGAGAAATTTACCTTGTGCTGCTTGAATGACCGAGAAATGCACTTGCCCACTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATACCGTGTGTCCTGTGGGTGGGGTGTGCGGAAGAAAGGAGCAGACTGAGGATGTGGCG
 TGTAAAGCAGTGTGCTCGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAGACATACACAGACTGT
 CTGAGTCAGAACCTGTGGTGTATCAAGCCGGGAGCCAGGAGACAGACAAAGCTGTGTGGCACACTCCGCTCTCTTC
 TCCAGCTCCACCTCACTTCCCTTGGCAGCAGCATCTTTCCACGCGCTGAGCACATGGAACCCATGAAGTCCCT
 TCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAAATCCAATCTTCTGCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGACAGCTCCCTGACAAACAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAAGCCCTC
 CAAACCTTCAGGTATCAACCAACAGCAAGGCCCCCAACACAGACACATCTGGAAGCTGCTGCCGTCCATGGAG
 GCCACTGGGGCGAGAAATTCAGCAGCGCCATCAAGGGGCCCAAGAGGGGACATCTTAGACAGAACCTACACAG
 CATTTTGAACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGATTGTGGTG
 TGCAGTATCCGGAAGAGCTCGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAGAGGCA
 GGGCTGAAGAAATCCATGATCTCAACCCAGAACCGGGAGAAATGGATCTACTAGTCAATGGCCATGGTATCGAT
 ATCTGAAGCTGTAGCAGCCAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTGAATGCCAGTGAAG
 AGGAGGTGTGCTTCTTCCAATGGGTACACAGCGCAGCAGCGGGGCTACGAGCTCTGACGACATGGAGC
 ATCCGGGGCCCGAGGCGAGCTCGCCAGCTAATTAGCGCCTGCGCCAGCACCGGAGAAACGATGTGTGGAG
 AAGATTGCTGGGCTGATGGAAGACACACCCAGCTGGAAATGACAACTAGCTCTCCGATGAGCCCCAGCGCG
 CTTAGCCGAGCCCCATCCCGAGCCCCAACGCGAACTTGAGAAATTCGCTCTCTGACGCTGGAGCCTTCCCCA
 CAGGACAAAGAACAGGGCTTCTTGGTGAATGAGTCGGAGCCCCCTTCTCGCTGTGACTCTACATCCAGCGGCTCC
 TCGGCTGTAGCAGGAGCGGTTCTTTATTACCAAGAAAGAAAGGACAGACTGTGTGGCGGTTATCGCCGTGAGC
 CCTGTGACTCTGACCTATCTTTGATGACATGCTCCCACTTTCTAAATCTGAGGAGTCCGAGGTGATTGAAGAG
 ATTCCCGAGGCTGAGGACAAACTAGACGGGCTATTGCAAAATATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCCTGGACTCTGTTTATAGCATCTTCTGACCTGCTGTAGAACATAGGATACCTGCAATCTGGAATTAATCA
 ATTAGTGTGCGAGGTGCTTTTAAATTTCTTCTGTTCTGATTTTGTGTTGGGCTGTGCTGTGTTGT
 GTGTGTGCTGTGCTGTGTGTGTTTAAACAGAAATATGGCAGTGTGAGTTCTTCTCTCTCTC
 TCTCTCTCTTTTCTTAAATTAACCTCTCTGGGAAGTGGTTATAGCCCTTGCAGGTGATCAATGTTGTGAA
 ATACCCACCACTAAAGTTTAAAGTTCCATATTTCTCCATTTGCTCTCTTATGATATTTCAAGATTTATCTG
 TGCATTTTAAATTAATCAATTAACATAAATGCAAGTGTGACTTTTCCACACATCGGATGTGGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCTATAAGCAGTCTTATGTCTCTTAACATTTACACCTACTTTTT
 AAAAAACAATATTATTACTATTTTATTATTGTTTGTCTTTTATAAATTTCTTAAAGTTAAGAAAAATTAAGA
 CCCCATTGAGTTACTGTAATGCAATCAACTTTGAGTTATCTTTAAATATGTCTGTATAGTTTCAATTTATG
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTCACCTGGACACCGGTAGAAATGCTTGAATTAATCTG
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAATCTCAAGCCATCAGGATTTGCTATTTAAAGTGCTT
 GACAACTGGGCGACCAAGAACTTTGAATCACTTTTAGGATTTGAGCTGTTTGTGAACACATTTGCTGCACTTT
 GGAAGTCAAAATCAAGTGCCAGTGCGGCCCTTTTCATAGAGAAATTTGCCAGCTTTGCTTTTAAAGATGTCTTG
 TTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCTTGGCTGCTGGGATTCCTTACCAATTT
 ACTTTTAAATAAAGTGGCTGCACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAGAT
 TACCTTTTAAAGTCTGACTTGGCAGTTTCCAAAGTTCCAAAGTGGCGTGGACTTTTGTGTGGGTGGGGTGTGG
 GTAGTGTGGAAGGACGATATCAGAAAAATGCCTTCAAGTGACTAATTTATTAATAAACATTAGGTGTTTGTGA
 AAAAAAAA

00973293-101501

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHC'TNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGGVRRKGTETEDVRCKQCARGTFSVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAFAFNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLEFIIGVKSQEASQTLSDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

00975208.101504

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTGAGAGGTCTCGAAATAGTCAC
CATGGGGGAAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAAATAAGTCCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACCTGCTGCCATTGAAGTTTTTCCCAATCATCGTCAITGGGATCATTGCAATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTCCAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCTGTGCCAAC
TGGGTTTTCCCAAGCTATGTGAGTTACAGATAACCTCAGAGTGAGCTCGCTGGAGGGGACGTTT
CGGAGGAGTGTGTGTCCTCGATCACCTCTGGCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT
GTGGTCATAGAAGGGGTACAGCTACGCTACGCTCGTGGGTGGAACATGCTTGCTCTCGCAG
TGGCCCTTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACTGTGCGGGGGCTCTGTCTATCAC
GCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACCTGGTGGAGAAG
ATTGCTTACCACAGCAAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCAGTTTCAATGAAATGATCCAGCCTGTGTGCTGCCCAACTCTGAAGAGA
ACTTCCCCGATGGAAGAGTGTGCTGGACGTCAAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCTGTCTGTAACACAGCGGCCGTCCCTTTGATTCCAAAGAGATGTGCAACACAG
GGACGTGACGGTGGCATCATCTCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGGTGTACAC
CCGTGTCACTTCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCGATCCTCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCGAAGAGAGGCACCCTTCCATCTGATTCAGGCACAACCTTCAAGCTGCTTTT
GTTTTTTGTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCACTGGCGAAA
TCCTGTCTCACTGCAGCCTCCGCTTCCCTGGTTCAGCGATCTCTTGCTGACGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCAACTAATTTTTGTATTTTTAGTAGAGAC
AGGGTTTACCATGTGCGCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTT
CAGCCTCCACAGTGTCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTACGCTCCTTTC
TGATCTTCACTAAGAACAAAAGAACGCAACTTGCAAGGGCGGCCCTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAGGCCACCAACAGCCATCAGAAAAGACGCCACCGCCAGAAAGTGCAGAAGTGCAGT
ACTGCACGTTTTTCTCTCTAGGACACAGAACCAACCCACCTTTCTACTTCCAGAGCTTAT
TTTCACTGTGGGAGGTTTATCTAGGAATGACTGTTTAAAGCCCTATTTTCACTGATTCTT
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAATAATATGTTTCTCTCCCT
CATGTCTGCGGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

00973398.101501

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDGGGLVCQERRLWKLVGATSFSGIGCAEVNKPQGVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

105102 0000000000

FIGURE 29

CCCACGCGTCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGTGTCATTTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGGCGCACGACAGCACACACAGGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA
 GCTCAGCGCGGCGCGCGCGCGCTGCGCGAGGGGCTCCGGAGCTGACTCGCGCGAGGCGAGGAAATCCCTCCGGTGGCGA
 CGCCCGCGCCCGGCTCGGCGCGCGCGTGGGATGGTGCAGCGCTCGCGCGCGGGCGCGAGAGCTGTCGCACTGAAG
 CGCGCGGACAGTGGGACGCGCGCGCTGCGCGCTGTCCCCCGCGCGCGCTCTGCTCGCCCTGGCGGGTGCTCT
 GCTCGCGCGCTCGGAGCGCGCGAGGGGTGAGCTTTATGGAACTCAAGGAAGAGCTGATGAAGTTGTCACTGCTCTGT
 TCGGAGTGGGACCTCTGAGTCCGAGTGAAGAGCTTGCAGTCCAAGAATCATCCAGAAGTGTGTAATTTGAGCT
 ACAACGGGAAGCAAGAACTGATCATAAATCTGAAAGAAATGAAGGTCTCATTTGCCAGCAGTTTCAACGGAAC
 CCACTATCTCGAGAACGGTACTGATGTCTCCCTCGCTCGAAATTAACGGGTCACTGTTACTACCATGAGCATGT
 ACGGGGATATTCTGATTTCAGCAGTCACTCTCAGCACGCTGTTCTGGTCTCAGGGGACTATTGTGTTTGAAGATGA
 AAGCTATGTCTTTAGAACCAATGAAGAAGTCAACCAACAGATACAAACTCTTCCAGCGAAGAAGTCTGAAAGCGT
 CCGGGGATCATGTGGATCACATCAACACACCAAACTCCGCTGCAAGAAATGTGTTTCCACCAACCTCTCAGAC
 ATGGGCAAGAAGGCATAAAAGAGAGACCCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAAACG
 AGAGTTTCAGAGGCAAGGAAAGATCTGGAAAGAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA
 GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCACTTCCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA
 TGACAAATCGCAGCTTGTGCTAGTGGGTTTATTTCCAAGGACCAACATCGGCAATGGCCCCAAATCATGAGCATGTG
 CACGGCAGACCACTCTGGGGGAATTTGTCATGGACCAATCAGACAAATCCCTCTGGTGCAGCGGTGACCTGGCA
 TGAGCTGGGCCCAAAATTTGGGATGAATCATGACACACTGGACAGGGGCTGAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
 GGAGACCAAGCTGGAGAAAGGAATGGGGGTGTCCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTGGGGGCCA
 GAAGTGTGGGAACAGATTGTGGGAAGAGGAGGAGGTGTGACTGTGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCAACCTGTACCTTGAAGCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
 GAAGCCTCGAGGAACAGCGTGCAGGACTCCAGCAACTCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
 TCACTGCCAGCAATGTGTACTGTGACGATGGGCACTCATGTGAGGATGTGGACGGTACTGCTACAAATGGCAT
 CTGCCAGACTCAGAGCAGCAGTGTGTGACGCTCTGGGGACAGGTTCTAAACTGCCCTCGGGATCTGCTTTGA
 GAGAGTCAATTCTGCAGGTGTACCTTATGGCACTGTGGCAAGTCTCGAAGAGTTCCCTTTGCAAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCGCGCAGTCAATTTGATCAAAATGCCGTTTC
 CATAGAAACAAACTCCCTCTGCGCAAGGAGGCGGAGTTCTGTGCGGGGACCCAGCTGTACTTGGCGCATGA
 CATGCCGAGCCAGGCGCTGTGCTTGCAGGCAAAAGTGTGCAGATGGAAATCTGCCCTGAATCGTCAATGTCA
 AATATTAGTGTCTTTGGGGTTACAGAGTGTGCAATGCACTGCCACGCGAGAGGGGTGTGCAACACAGGAAGAA
 CTGCCACTCGCGGCCCACTGGGCACCTCCCTTTCTGTGAAGAATTTGGCTTTGGAGAGAGCACAGACAGCGGCC
 CATCCGCAAGCAGAGCAAGCAGCAGGAGCTCAGAGTCCAAAGGAGCGCGCAGGCGAGGCGCGTGGG
 ATCGCAGGAGCATCGTCTACTGCTCTACTGACACTCATCTAGCCCTCCCATGACATGGAGACCGTGACCACTG
 CTGCTGCAGAGGAGGTCAAGCGTCCCCAAGGCTCCTGTGACTGGCAGCATGACTCTGTGGCTTTTGCCATGTT
 TCCATGACAAACAGACACAACTGTTCTCGGGCTCAGGAGGGAGATCCAGCCTACCAAGGCACTGTGTCAGAAA
 CAGTGCAGGGAAGGGCAGCGACTTCTCGTGTGAGCTTCTGCTAAACATGGACATGCTTCAGTGTGCTCTCTGAG
 AGATAGCAGGTTACCACTCTGSCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
 ACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCAAGTGACACCTCAGCCT
 TGGCAGCCTGTATGACTGTGCTCTGCGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAT
 AGCAGGGTTTATGTTTAAATTTATCAGAGACCTGCCACCCATTCATCTCCATCCAGCAACTGTAATGGCAA
 TGAACAAATCTGGAGAGAGAGGTGAGGAGAAAGGGCGGTGAATCTGTGCTTTTGTGTCATGTGGACATGCGTGA
 AGTACTCAGGTTTGAAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCAACAACTCTTATTAAACAGTAAAGA
 TGTATAAAGTGAACAAATGTAAGACCTAACTCACTCCCGTGGCCACTTATGCAATAAATAGAGTGCATT
 GAAT

09973293-101501

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYHGHVVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTFNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIETIANHVDKF
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCINASTGYPPPMVFSSCSRKDLTSLEKGMGVCLFNLPEVRESFQGQKCGNRFVEEGEE
CDCGEPEECMNRCNNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGICYNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRIILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRNKCHCEAHWAPP
FCDKFGFGGSTDSPIRQAEARQEAESNRERGGQGEFVGSQEHASTASLTLLI

Signal peptide:

amino acids 1-28

00973229.101501

FIGURE 31

TCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAAGTTTGGCCTTTCAGTGAAGCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

09978298.101501

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

105101-922269

FIGURE 34

GC CGCGGGCGAGAGCGCGCCAGCCCCGCGGATGCCCCGCGGCCAGGACGCCTCCTCCCGCTGCTGGCCCGG
CGCGCGCCCTGACTGCGCTGCTGCTGCTGGGCTGCTGGGCGCATGGCGCGCGGGGCGCTGGGGCGCCCGGGCCAGG
AGGCGCGGGCGGGCGCGCGGAGCGCGCCCCCGCGCGAGCGCGGAGGACGAGACAGGACCCGACAGCAAGCACC
TGTACACGGCCGACATGTTTACAGCAGCGGATCCAGAGCGCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTG
GACACTGCGAGCGGCTGCGAGCCGACTTGGAAATGACTGGGAGACAATACAACAGCATGGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCAACGCGCCACTCCGACGTGTGCTCCGCGCCAGGGGGTGGAGGATACCCCACTCTAA
AGCTTTTTCAGCCAGGCGCAAGAAGCTGTGAAGTACCAGGGTCTTCGGGACTTTCAGACACTGGAAAACCTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCGCGGAAGTGGAAACCGCCAGTGGCCCCGAGCTCAAGCAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCAGCTTGCAAGGCGACCACTTTTATCGGCTCTTCGCTC
CGTGGTGTGGCTCACTGCAAAAGCCTGGCTCCAACTGGGAGCAGCTGGCTCTGGGCGCTTGAACATTTCCGAAACTG
TCAAGATTTGGCAAGCTTGATTGTAACAGCACTATGAATCTGCTCCGGAACACAGGTTTGGTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAAGTGGATCAGTACAAGGGAAGCGGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTGCAGCTGCAGCGCACAGAGACTGGAGCGACGAGAGCCGTCACGCCCTCAGAGGCCCGGTTGCTGGCAG
CTGAGCCCGAGGCTGACAGGGCACTGTGTGGCACTCACTGAAAATAACTTCGATGACACCAATTCAGAGAAGGAA
TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTGGGAGGAACCTCTTA
AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCGAGGAGGGGAAGAAAGTCAGTGAGCACAGTGGAGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAAGCGAAGAGCAACTTTAGGAACACAGTTGGAGGTGAC
CTCTCCTGCCAGCTCCCGCACCTTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTCCAGAAAGCAACATACTAAGCGTGAAGTATCTTCTTTGTGTGTGTTTTCGAAGCCACACACTCTACAG
ATTCTTTTATTAAGTTAAAGTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA
TATCCCTTTGACCTTCTCTTGAAGAAATTTAATGCTTCTCTTGAAGTAAAATAGCGTTGAGGGAATGAAA
TATCTTTTATTAAGTTAAAGTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA
CCACAGAGTTCTGGAAGGTGGCCCTTGTGCAAGTATTGACGTTCTCTGATCTTAAGGTCAAGTGTGACTCAATAC
TGTGTTGTCCTGTAAGGTGCGCTTGTGCAAGTATTGAAATGCAAAAACCAACCTCTGGAAGATACCTTCACGGCGCGTGC
TGGAGACTCTGTTGCTGTGAATATCTCTCAGGTGTGAGAGGTAGCCGTGATGAAGACAGCGGTTACTTCTGACC
GTGCTCGATGAAGAGAAAGTGTGATGCCATAACTTATGTGTGATACTTGTCAAATCAGTACTCTGTTCAAGGGAT
CCTTCTGTTTCTCAGCGGGTGAACATGCTTATGTTCCCTCATGTTAAACGGAAGCCAGAGCCACATGAATGT
TGGATGCTCTCTTAGAAGGGTAGGCAATGGAATTCACGAGGCTCATTTCTAGTATCTCATTAATCTAATGTA
AAGATTCCAGTTGTATTGTCACCTGGGGTGACAGACAGAGCGCTTCCAGGCCCTGGGTATCCAGGGAGGC
TCTGAGCCCTGCTGAAGGGCCCTAATAGAGTTCTAGAGTTCTGATTTCTGATTCAGTATGCTCTTTAGAGG
CTTGCTATACTTGGTCTGCTCAAGGAGGTGCACCTCTAATGTATGAAGAATGGATGATTTGATCTCAAGAC
CAAAGACAGATGTCACTGGGCTGCTCTGGCCCTGGTGTGACGCGCTGGCAGCTGTTGATGCCAGTGTCTCTTA
ACTCATGCTGTCTTGTGATTAACACACTCTATCTCCCTTGGGAATAAGCACTACAGGCTTAAGCTTAAGATA
GATAGTGTGTTGTCTTTTACCATCGAGCTACTCCCATATAAACCACCTTTGATCCCAACACTCTTACCCCACT
CCCATACGCAAGGGGATGTGGATACTTGGCCAAAGTAACCTGTTGGTAGGAATCTTGAAGAACAGAACCACTATA
CTGCTGTCTGAGGCGAAGATAACAGAGCATCTCGACCAAGCTTCTGCTTAAAGGAAATCTTTATTAATCAGG
TATGGTTCACAGATAATCTTTTAAAAAAACCAACTCTTAGAGAAGCAACTGTCAAGAGTCTTGTACA
CACACTTCAGCTTTGATCAGAGTCTTGTATCCAGAAATCAAAGTGTACAATTTGTTGTTTACACTAT
GATACCTTCAATAAATCTTTTTTTTAA

00973293.1.1501

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLP LLARPAALTALLLLLGHGGGGRWGARAQEA AAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFPQGQEA VKYQGPRDFQTLNWM LQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSA SNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHVELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLES LREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFPYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLFRGGKKVSEHSGGRDLD SLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTCACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGGCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTACTATGTTGC
CAAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGGACAGTACA
TGTTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTIGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

09978299-101511

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEG
KHGKVGRRMGPKGIKGEIGMDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDCCRY
RKFFVGQLDISIARLKTSMKFVKNVIAIGIRETEEFYYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQYNYSNWNNEGEPSDPYGHEDC
VEMLSSEGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

10597: 62260

FIGURE 38

GGTTCTATCGATTGCAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGCGTGT
GCCAGCGCAGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATCTTTGCGAGCGGCTGGAACACGAGCGTGCAGATAGAGGAAGC
GGGCTCCATGGCTGCGCTCTCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCGACCTGGCCTGGCGCCTCGCGGAACTGGCCAGCAGCGCGCCGCGC
ACACCTTTCTCATTACGGCTCGCGCGCTTTAGCTACTCAGAGCGGAGCGCGAGAGTAAC
AGGGCTGACAGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGAGCCGACGCGCGCGACAG
CGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGAGATGACGCGCGCC
GAAGCGCGCGGAGTTTGCCGGAGGGGACGCTGCCGCCAGAGGTGGAGGAGCCGCCCCCT
CTGTACCTGGAGCACTGTGGCGCTGCTCTCTCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCCGGCTGGCCAAAGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCTCCGAGCTCGCGCGCGCGCGCTGGTGTCTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCGGACCTGCCGCCCTGAGAGCCATGGGCTCCACCTGTGGGCTCGAG
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCTGTACATCTTC
ACCTCTGGCACCCAGGGCCTCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCGGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCAGATG
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAGAGGCGAG
AACGTGGCCATAAGGTCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGAGCGCT
TTTGTGCGCGCTTCGGGCCCTGCAAGTGTCTGGAGACATATGGAAGTGCAGAGGGCAACGT
GGCCACCATCACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTCTCTGGCTTTACAAGC
ATATCTTCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAAATCGGGACCCC
CAGGGCCTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCATTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCACAGGGGAAGTTGCTAAAGG
ATGTCTTCCGCGCTGGGATGTTTTCTTCAACACTGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAATGTGGC
CACAAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTCAGGAGGTGAACGCTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTTCTGCGTCCCCC
CAGCTTTGGACCTTATGCACTCTACACCCACGTGCTGAGAAGTTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCAGGAGTCTTTGGCCACCACAGAGACTTCAAAACAGCAGAAAG
TTCGATGGCAAAATGAGGGCTTCGACCCAGCACCCTGTCTGAGCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCTACTGCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGTGGGG
CCGTGTCAGGTGTACTGGGCTGTGAGGATCTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAGGAAAAAAGG
AAAAAAGGAGGGCGCGCACTCTAGAGTGCACCTGCAGTAGGATAACAGGGTAATAAGC
TTGGCCGCATGGCCCACTTGTATTATGACG

Figure 1. The structure of the proposed model.

><MW: 78644, pI: 7.65, NX(S/T): 2

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
 CACATCCCCAAGAACCCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTTCGCTCTC
 GCTTTCCTCATCTCCCTCCCGGGGAGCGCGCGCGCTCCACCTTTGCCCGCACACTCCGGC
 GAGCCGAGCCCCGAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCACTGTGAACCC
 CCATGGTGGTTTTTTAAACACTTCTTTTCTCTCTCTCTCTGATTGCACCGTTTCCA
 TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGCCATCGT
 CCATCTGGCTTATAAAGATTGTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG
 CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCGCTGCTCTGGCGGGCTTT
 CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCGCTGGGGTTTTACCGAGCTGGATTGTATG
 TTGCACCATGCTCTTCTGGATCGGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC
 TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCCGCCAGGCGTACGGTGCC
 AAGGGATTGAGCTTGGCGGACATCCCTACAGGAGATCGCAGGGGAACACTTAAGAATCTG
 TCTCAGGAATATACATGCTGCACCAACAGAAATGGAAGACAAGTTAAGCCAAACAAAGCAAC
 TCGAATTTGAAAACCTTGTGGAAGAGACAAGGCCATTTTGTGCGCACCACTTTTGTGTCAGG
 CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
 TATGTTTGTACGGACCTATGGCATGTGTACATGCAAAATCAGAAGTCTTCCAGGACCTCT
 TCACAGAGCTGAAAAGGTACTACACTGGGGTAATGTGAATCTGGAGGAATGCTCAATGAC
 TTTTGGGCTCGGCTCCTGGAACGGATGTTTCACTGATAAACCTCAGTATCACTTCAGTGA
 AGACTACTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
 GGAAACTGAAGATTGAGTTACCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
 ACTGTGGGCAGAGAAGTTGCAAAACCGAGTTTCCAAGGTGAGCCAAACCCAGGGTGTATCCG
 TGCCCTCATGAAGATCTGTACTGCCCATACGTGCGGGGCTTCCACTGTGAGGCCCTGCA
 ACACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
 TGGAACTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
 TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
 ACAGCATGAGGTGTCTGCAAAAGGTCTTTCAGGGATGTGGTCAGCCCAACCTGTCTCAGCC
 CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTAATAACGTTTCAGGCCCTACAATCCTGA
 GGAAGACCAACAACCTGCTCAGGCACAAAGCTTGGAACCGGCTGGTCAGACATAAAAGAGA
 AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCCTACACTATCTGCAAGGACAGAGC
 GTGACAGCGGGCACGCTCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
 GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCGAGGTGGATGTGGACA
 TCACTCGGCTGACACTTTTATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
 CTAAAAACCGCTACAAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
 CTCAGGGAGTGGCAGTGGGTGTCATGGATGACGTGTGTCCACGGAGTTTGTAGTTTGTCA
 CAGAGGCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTTCGACGCCAGCGTGGC
 CACTCCCTGCTCTCTGGTCTCTCACTGCAATGTCTCTGCACTGACAGAGACTGTGACAGTA
 ATCTGGGTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTCTTT
 TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACGGTTTTCTATGAGAAGAGAG
 CAGTAATGCAATCTGCCTCCCTTTTGTTCCTCCAAAGAGTACCGGGTGCCAGACTGAAGTCT
 CTCTCTCTCTCAGCTCTCTGTGGGACCTTGTATTCTAGAGAGAACTCTTACTCAA
 ATTTTTCTGACAGGAGATTCTTCTACCTTCATTGTCTTTATGCTGCAGAAGTAAGGAAT
 CTCACGTTGTGAGGGTTTTTTTTTCTCATTTAAAT

0973293-101501


```
><subunit 1 of 1, 555 aa, 1 stop
```

MPSPWIGAVILLPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVBETHSHFVRTTFVSRHKKFDEFFRELLENA EKS LNDMF
VRTYGM LYM QNSEVFQDLFTBLKRYTYGGNVNLEEM LNDFWARLLERM FQLINPQYHFSE DY
LEC VSKYTDQLKPF GDVPRKLKI QVTRAFIAARTFVQGLTVGREVANRVSKVSP TPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNV MKGCLANQADLDTEWNLFIDAMLLVAERLEGFPNIES
VMDPIDVKI SEA IMNMQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLDRIEIKELKLSKKVWSALPYTICKDESVTAGTSNEECCNNGHDSKARYLPE
IMNDGLTNQINNPEVDVIDITRPDTFIRQIMALRVMTNKLKNA YNGNDVNFGDTSDESSSGS
SGSGCMMDCVPTFEFEVFTTEPAVDPDREVDSSAAORGHSLLSWLTICVLVALORLCR

amino acids 1-23

FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGCCTTGAAGAATATATTTCTTGGTGAATTTTGTATGTCGTGTCATATGA
CACTTGGGTTTTTTAATTAAATCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAATAAGAATGTTTGAGCACACTGCC
ACAAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTGTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTCTGTCATACCATTAGAAGA
ATTTTATTTTCATTTCCTCAAATATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATATGTTTGTGTCAGAGTTGAGACAACCTTTATGTTTCTATCATAAACTATTTATGTCATCTT
AATTATTAATGATTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAT
GTATCATTTGGTCTTAAAAATAAAAAATCTTTACTAATAGGCAATGAAGGAATGGTTTGTAAACACCCACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCAATAATAACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCATTAAAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCCTGGAGTAGGTAACTTGTCTGGAAACCCC
ACATGCAAACTCATGAGGAGAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATTTGGTGTGGATCCTGTAGACCTGGTGTTCCTTTGAAGTGCCCTCTCCTAATGTCAGAGGCCTTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTATATCAC
AACTCAAAGGACTGTGATATAATCCATTATATCACAGCTCACAGTTTCTGAAAATGTATAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATGGGTAAAGATGATTTAAATGATTTTAAATTTTAACATTTTATTCTAGAAATATAT
GGCTCCATTTTATTTATAGTGTAAGTTGTATTTCCTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA
AAA

CG97329.101501

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCTCTTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCTCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTGAGCCT
GGGGTCTGTCACTATGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACTGGATGTAAGTTTGGTGAGTGGTGGGACCAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAACCTGCAGTCAAGATGTAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGTCTTTGCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGTGAGTACAGCTGTGGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTTGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAAATGTCACA
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCGAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGATATAAAGGCAATGGACTTCGGTGTCTTGCTATCCCTGAAAAATCTTG
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGGCAAAATTTAAAAATGTTACCCAGAACCCACCAGGACTCC
TACCCCTAAGGTGAACCTTGACGCCCCCTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAT
CTCATGGAGGTAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGCATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCAGATAATGCTATGGC
TTCTATATGGCAGTTCCGGCCTTGCCAGGTCAAGAAGACATTTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACGGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAACAAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAATTCAGTTGTATCAAGGAACGTATGC
TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTCAGGCTTATGTCAGATAGCCTTTTATCTGTGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTGCTCAGTTCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAAATTAAGTGTGAAAAATTTGTAATGTACCAACAGAAATATTATTG
TAAGATGCTTTCTTGTATAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAGACACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGGA
AACTATGACATCAAGATAGACTTTTGCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATCTTTGTAATAATAA

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FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE
ATCEPGCKFGECVGPNNKCRFPGYTGKTCSDVNECGMKPRPCQHRVCNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRVCNFTGSIYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGACGCAGAAGAGTGCAT
GAGCTGGAAAGGTTGAAAAGAAGATGCCCTAGAGAATGGCAATTTAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTG
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATGAAGCTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

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FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVVWTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTTKIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

0073208 101501

FIGURE 48

GCGACGTGGGCAACGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCCG
 TTGCATCTTTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGGCTCTGTCC
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC
 TTCGTGCTCTATGATTTCTGCAATTGTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
 ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
 GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCTCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
 CGAGCTCGCCCCACCCACGACCCACACACCCCTCTGCTGCCCCAGCCCCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCGATGATGCTCTCTGGGACC
 CTAGCCAATCTGCGCCTGCGTCTCATCAGTGCGCCCACTGTAACTGTATCTACAACAGCT
 GCACCAAGCAGACCTGTCCAACCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
 GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGCCCTGTGCTGTGCTCGAGCTGACGGA
 CACTGGGTTCAGGCTGGCATCATCAGCTTTGTCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
 GCTGTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTTCAGGGGGCAGCTT
 TCCTGGCCCAGAGCCAGAGACCCCGGAGATGAGTGTAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT
 GATGCACCAAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGGAGGGCGGTGCTAACTG
 CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGAACAGA
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCTGTCATGGAGCCTACACCCACCTGAGGGGGG
 CTAGCAGATGGCCCTCTGTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
 TCTGCTGCCCTATCTGTACCACCACTGCTGTGAGGGAGCGTGGCTGGGTTCTGGGACGG
 GCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCTCTCTGGGGCCCTAG
 GGCCTGCAGCCGGCTGCATGAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
 TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCTGTCTGGGGCAACCATGGTGT
 CATGAGGTGAGGGGCACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
 CCCCAGGAGGCCCGCGGTCTTACCGCGCTCCCTGCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
 AACATAAGCCAAACCAACAGCTGCTGACAGAGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAAATGGCATTACTGCCCTGTCTCTCCACCCCTGTCTGTGTGATTCCAGGCAC
 CAGGGCAGGCCCCAGAAGCCAGCAGCTGTGGGAAGGAACCTGCCCTGGGGCCACAGGTGCCCA
 CTCGCCACCTCTCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
 AGGCGTCTCAGCTTTCTCTCTCTTACTCTTTTACATACAATCACGCCAGCCAGCTTGT
 TGAAAAATTTCTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAAACTTAAATAAATTTGTATC
 AAAATAAAA

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MLLSLSVSLAGSVYLAWILFFVLYDFCIVCITTAYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTVWLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
BEVGVAAQLPRAYNHYSQSGSDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPGQPGVQGPCQDSSGGFVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGLACGGALVSEEAULTAAHCFIGRQAPEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYPDHHLDPDGERG
WVLGRARPGATISSLQTVPTVTLGPRACSRHLHAAPGGDGSPIILPGMVCTSAVGELPSCEGLS
GAPLVEHVRGTWFLPAGLSHFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEPEPEABP
GSLCANISOPTSC

Signal peptide:

amino acids 1-15

amino acids 79-95, 343-359 and 237-247

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCGCCCCCATTCGGGCCGGGCCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCAGAGTCGGCGCGGCGCGGCGAGGGGAGCCTTCCACCACGGGGAG
CCCAGTGTGTCAGCGCCCTCACAGGAAGATGCTCGCTGCGCGGGGCGAGCCCTGGCATGGGTGT
GCATGTGGGTGTCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGTCTCTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAAACA
GCTGTGTGCACAGCTTTGTGTGAGGGCCAGGACCAGGGCAGCGCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGTCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGTCAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAAACGA
GCAGGGCTTGTGTTGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCGCAACCCCGTGTCTGCAGCAGGATGCGCACRGCTGTGTACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG
GAGCTGTACCCCTCCCTACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACCTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTCTCCAATGGACATGATTCCAAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCCTTTTTTCTCCAAAAGATGCAATATTGAGA
CTGACTGACCCCCCTGCCTTATTTACCAAAGACACGATGCATAGTACCCCCGGCCTTGTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGGCGCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTT
CCCTCCTTCTCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCAACCCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCTCTGGCCAGCTCCTGGCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCTTCCG
GATGTCTCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAAACTGGGGGTATATTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGS PGMGVHVG AALGALWFCLTGALEVQVPEDFVVALVGTDTATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQRRVVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDGGQVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTPFPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEKSKTALQPLKHSKSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
 CTGAACCTTGCTCTGAAGCCCTTTGTCCGTAAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
 AGGGACCTTTTCGTGCTTTTGTAGGGAATCTTTCTTGCTTCAGCAACATGAGGCTTTTCT
 TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
 GAAGTGAAAATGAAGTTCTCCAGAAGCCATTCACTGCCATCGCAAGACCAAGGAGGGGA
 TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTCACTCCAATC
 ACAACATAAACAATGGTCAGCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
 TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTTCCCTCTGC
 TCTGGGCTATGGAAGAAAGGAAAAGGTAAATTTCCCCAGAAAGTACACTGATATTTAATA
 TTGATCTCCTGGAGATTGCAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT
 AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
 ACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAG
 AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACCGATGAGTTA
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
 AGAACATTTTATTTTATACAAATGTTCTTTCTGCTTTGTTTTTATTTTATATATTTTTT
 CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT
 GGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACCTTTACAG
 ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
 ACGACATGAGACCAAGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC
 TCCAAGTTAGAGGTCAACATTTGAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
 GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
 TGGTTGTTGGACCTGACTGTGTTAATGGCTACTGCTTTTACTAAGGAGATGTGCAATGCTGAAG
 TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAATCCAGCACTTTGGGAG
 GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
 CCCTATCTCTACTAAAAATACAAAGTAGCCGGCGTGGTGTGCGTGCTGTAATCCAGCT
 ACCAGGAAGGCTGAGGCGGCAGAAATCACTTGAAACCGGAGGCGAGGTTGCGGTAAGCCGAG
 ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAAAAAGAACACGGTTAATACCATATNA
 ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGT
 TGGTGGCCTATTATGATAAATAGGACAAATCAATTATGTGTGAGTTTCTTTGTAATAAATG
 TATCAATATGTTATAGATGAGGTAGAAAGTTATATTATATTCATATTTACTTCTTAAGGC
 TAGCGGAATATCCTTCTCGGTTCTTTAATGGGTAGTCTATAGTATATTATACATAACA
 TTGTATCATAAGATAAAGTAGTAAACCAAGTCTACATTTCCCATTTCTGTCTCATCAAAAC
 TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
 TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAAATGGTGAACCTTGTCCTCTA
 TAAAAAATACAAAATTAGCCAGGCGTGGTGGTGACACACCTGTAGTCCAGCTACTCGGGAG
 GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGAGGTTGCAGTGAGCCAAAGATTGTGCC
 ACTGCACTCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGACAGA
 CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

09978298-701501

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Abstract**
 12. **Summary**
 13. **Key Words**
 14. **Keywords**
 15. **Subject Headings**
 16. **MeSH**
 17. **Indexing**
 18. **Classification**
 19. **Numbering**
 20. **Ordering**
 21. **Grouping**
 22. **Labeling**
 23. **Marking**
 24. **Notation**
 25. **Symbolism**
 26. **Diagramming**
 27. **Flowcharting**
 28. **Mapping**
 29. **Charting**
 30. **Graphing**
 31. **Tablemaking**
 32. **Formmaking**
 33. **Diagrammaking**
 34. **Flowchartmaking**
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 231. **Mappingmaking**
 232. **Chartmaking**
 233. **Graphmaking**
 234. **Tablemaking**
 235. **Formmaking**
 236. **Diagrammaking**
 237. **Flowchartmaking**
 238. **Mappingmaking**
 239. **Chartmaking**
 240. **Graphmaking**
 241. **Tablemaking**
 242. **Formmaking**
 243. **Diagrammaking**
 244. **Flowchartmaking**
 245. **Mappingmaking**
 246. **Chartmaking**<

```
><subunit 1 of 1, 211 aa, 1 stop
```

MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNGQPIWFTLTGILEALKGWDQGLKGMCVGEKRKLIIPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Signal peptide:

amino acids 1-20

amino acids 176-179

amino acids 143-146, 156-159, 178-181 and 200-203

amino acids 208-211

amino acids 78-114 and 118-131

amino acids 191-203, 184-203 and 140-159

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTAGCAT
CCAAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA
CTAACATCTCAGTCTCTGAAAAATGCACAGAGATGCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACACGATC
CTGCCACCTCAACGTCTCAATGGCTCTGACGCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAAGCTGGAGCGGTTTTCAAG
ACCGCGTGGAGTTCTCAGGGAAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACGTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATGTGGGTGCCTCCGTGCGGGGCTTCCTGGCTGTGGTCACTCTTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAAGTATGGGTGGCCGGCC
CTGCAGCTCCCGTGTCCGCTCTCCTCCCCCTCTCGGCCCTGTACAGTGACCTGCTCTGCTCG
CTCTGTGTGCTTCCCGTGACCTAGGACCCAGGGCCCACTGGGGCCTCCTGAACCCCG
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG
GGGAGGCAGAGGACATGTGAGGGTCCCCAGAGAGAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCCGTGTCACTGCCCCAGTGCTTGCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTGTGTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
TGCTCTCCCTGCTCCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGATTCAGGGCACTGACGGAAGCCAGGG
CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCTCCTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGTTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGAAGGGAAGCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGCTCTCTCCAAACAACTCCCTTCGTGGGGACAAAAGTGACAATTTGATAGGCCAGGC
ACAGTGGCTCAGCGCTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAATAACAAGAAATTAGCTGGGCGTG
GTGGCGTGTGCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAACTGAGATAGTGAAGTGCACCTGCAATTTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

00973223.101501

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNLVNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

10973223401501

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAAC TGCTACATCATGAACCCCC

097629-10161

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

0973298-101501

TGCGGCGACCGCTCGTACAAATAGGGGCTCCACCTCCGCTCCAGCTGTGGGGCTGTCCCGGATGGCCCTCTCTGTCTCTTGTGCTGCTAATCACTGCTTCGCGGACCCAGCGCTCCGCGCGAGCTACCCCCAGTGGTGTGTGGTCTCTGGTGAATTTGGGTAAACAGTCTGGAGCGGACGTGGACAAGCCGACAGTGTGTGCATACCTCTCTCTCCAGAAGA CCGAAGAGCTACTTCCAAATCTGGCTTGAACTGGAACTGCTGCTGCTGTATCATATGACTGTGATGTACAATA TCAGGCTGGTTTGAACAACAAATACCAAGGGCACCCAGTTTCTGATGGTGTGGATGTACGCTGTCCCTGGCTTTTG GCGAGACCTCTCTCACTGGAGTTTCTTGAGACCCGACCAAGGACCGAGTGGGTTCTATTCTCCACACATGGTGGAGA GACTTGTGGGCTGGGGCTACACAGGGGTGAGGATGTCCAGAGGGGCTCCCTATGATGCGCCGAGGCCCAAT AAAACCGGGCCCTACTCTCTGGCCCTCCGCGAGATAGATGAGGAGGATGTACAGCTGTGTGGGGGCCGCTGGTGTG TGGTGGTCCACAGTATGGGACAATGTACACGCTCTACTTTGTGACGCGAGCCGCGAGGCTGGGAAGACAAGT ATATCCGGGCTCTCTGTCTCACTGGTGGCCCTTGGGGGGGCGCCGACGACGCTGCGCTCTGGCTTCAGAG AACAAACACCGATCCAGGTACTGGGGCCCTGAAGATCCGGGAGCAGCAGGCTCAGCTCTCTCACACAGCTGGC TGCTGCCCTCAAGTACATACATGGTCACTGAGAAGAGTGTCTCTGACAGACCCCAATCAATACATCACTCGGGG ACTACCGCAACTGTTCTTCAGGACATCGGCTTTGAAGATGGCTGGCTCTATGCGAGACACAGAAAGGCTGGTGG AAGCACAAGATGCCACTGTGGCTGCGATCTGCATCTCTTATGGTACTGGCGCTCCCAACCCAGCATCTCTTCACT ATGAGAGCTTCCCTGACCTGTGACCTAAATCTGTCTTGTGACGCGCATGTGATCTGTAACTTGAAGAGTGCCC TGCAGTCTCCAGGCTCGCGCAGGCGCAGGAGCACAAAGTTGTCTGTGACAGGATCTGCGCAGGACGAGCATCG AGATGTGCGGCACGCCCACTCCCTGGCTTCTGAAAGCTGGTCTCTTGGGCCCTGCACTGCTGCCACAGGA CTCTCTGTGCTCGGCCCTGGACCTCTGTGGCCCTTGGGGCTTATGGCCCGACGGGTTTCGAAAGTTTGTG TCACCAATTCAAGGCCCGAGTCTTGGATCTGGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCTTCTCTCT GTGGCAGTGAAGAAGGAAGAAATCAGAGTCTAGACTCAGAGGACATCGATGAGGAATGTGCTGATGGGTGGA ACTGCTCTGTGACCTTAGAGCTCTGGCTCCACAGGSGTGACTGGCGGCCCTGTGCCAGTCTCGGTGTGAGCTTCTGTGCCCTATTCTCTGTGGGCTTTTCATACTTGCCTATCTGACCGCTCGGCCCTGAGCTCTGCCATGATCTGAGGATGATCTGAGGCTGTGGCTGTACCCAGAGGTTCCAGGAGTCTGCCAGATAGGCTGCCATGTGATCGGTGATCGCTGAGCTGTCTGCTGCTTCCCTGTGAGCTTGGTGGCGAGCTTGACTGGCTCTGGGCGAGGCTGATAGTCTCTGCGAGCGGGCAGTTTGTGCTGTCTTCTGGCTTCCAGGCTCTGGGACAGATGTG CCCCAGTCCCGAGGCTGTGTTTCCAGGGGCCCTGATTCTCGGATGTGCTATTGTGCCCCAGCATGAAGCTGC TCTCCTTCAACCTGGGACTGTGGTTTCCAGAGTGAAGACAGGGGTTGGAGCACATGGGCTTCTGGGAACCTATGGA GAAAGGAAATCCAGGAAGAGCAGCCAGGCTGCTGCGAGCTCTCCCTGAGGCTGACCTCTTGCTACATCCCAACCATCA CTGACGCCACCTGCTAGGCTCTGCTAGTGAATCCTATGATCAAGTGGGTGAGCAGGAGGTGAGGATGGGGCTCTATTCACT CTGGGCGACCCAGCAGTGTAGTGTCTGGGACTAGCCAGAAATTTGAATGGGACCTGAGAGGACAGGGGTCCTCC TGAGGCCCCCTAGGGGCTTTCTGTCTGCCACGGGTGCTCATGAGTCTCCTGTGCGCAGGACATGGAGAT CAGGGCTGCGCTTCATGTCAGTGAATGCTCTTAAGTGGGTGCTGAGGAGCGAGGGTCTGAGGCTCTAGGT GGGGTTCCCAAGAGCGCTTCAAGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCGAGGCTGATTTCCTCTG TTGTCATACATGCTTGGCATCTGTCTCCCTCTGTCTGATGTGGCCCCATAGGGGCTCGAGCAGCTGTATCTGTG GATTCTGGCAATAAAAGTCTCTGATGCTGTAAAAAATAAAAAAAAAAAAAA

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPFYRVGLLPDGLLFLLLLLMLLADPALPAGRHPFVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGFVVLVAHSMGNMYTLYFLQRQPQAWDKYIRAFVSLGAPWGGVAKTLRVLASGDNRI
PVIIGPLKIREQORSASVSTSWLLPYNTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCC
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCTTGATCGTGTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTCAACCGCAACGAGGAT
GCCTGCGCTATGCGAGTGCCATCGGGGTGCTGGCCCTCCTGGCCCTCGGCCTTCTTCTTGGT
GGTGCAGCGCTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA
GCGGAGACCACCGAGGGCTACCGCGCGCCCTGTGTACTAGATGGCGGTTAGCGTGGGAA
GGGGACAGAGAGGGCCCTCCCTCTGCGCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA
GCCCCCTCTTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGTGGCAGAGCCACACCCCAAGTGCCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACCAGGCTCTTGTCCTCA
CTCAGGTTTGCTTCCCCTGTGCCCATGCTGTATGATCTGGGGGCCACCACCTGTGCCGGT
GGCCTCTGGGCTGCCTCCGTGGTGTGAGGGCGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTCCTGACAACACCAGCTTTATGTAAATATTC
TGCAATTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTC
TGTGCCAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

0976208-101501

<subunit 1 of 1, 224 aa, 1 stop

MESGAYGAAGAGGSFFLLRRFLTQPPVVARAVCLVFALIVFSCIYEGEGYSNAHESKOMYCVFN
RNEADACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIVIGDLLFSALWTLFWVFGFC
FLTNTQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYOOPFPPTONAETTEGYOPPPVY

Type II Transmembrane domain:

Other transmembrane domains:

N-glycosylation site.

amino acids 97-100

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLMSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLHASSCLWHLQGPKDMLML
KLRLLEWTLAECDRLAMVDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPFVVFQACEVNLTLNRLDSQGVLSSTPYFPSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTQGGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNLGCVFACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDCGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDICRDGSDEEHCD
CGLQGPPSRIVGGAVSSEGEWFWQASLQVGRHICGGALIAADRWVITAAHCFQEDSMASVTL
WTVFLGKVVQNSRWPGEVSKVSRLLHPYHEEDSHDYDVALLQLDHPVRSAAVRPVCCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCEAYRYQVTPRMLCAGYRKG
KKDACQGDGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGC GCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTACCGGGGCCGCTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGACAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCTGGGGTGCACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGTCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCGCCTGTCTCTGCACCCGTACCAACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTCTGCAGCTCGACCACCGGTGGTGCCTCGGCCGCGCTGCGCCC
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTTCAGAGCCCGGCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCCTATCGTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCACTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGGCTTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAAGTCCCCCTTGCAAAGCAGGGCCCACTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

00976293-101501

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCAGCCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAACACCAAGAGGTGGTTTTTGTTTTTTAA
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG
TTTCTGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACTCCTCCGACCTCCAAGGACCCAGAGCATGAAGGATGTACCTCTCCGTCCGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAACTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACAGCTTTACACGGA
TGGCGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCAGAGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGATGTCCCTCCACACCTACACGCGTTCCCTTCGGCTTGAGCATTGGTATTAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCCTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTAGAGGTAACCTTCAGTCCCTGGAGTGTCCCAGGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCAGATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAATCAGATTACACTGTGCATGTCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

097623.107501

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDVAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDVLVNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLCP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGGGCGGACGCGTGGGCCCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACTCTTCCCTCCCCCGC
TTCCCTGTGCGGCTCTCGCTTGGCTGGAGCGGCTGGAGGAGTGGAGCAGCACCCGGGGCGGCTGGGGGCTGACAGT
CGGCAAGATTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGCGAGGTGGCGACAGGGCCAGACGAGGGGCGCTCG
CTGCCGTGGGGGGCGGCTGTAGGCGAGGGCGCGCCCACTGGCGAGTGGCGAGCCCGGGGCTTCAGGAGCCCGCCCGGGAG
AGAGAGTGTGGGGCGGCGGAGCGAGGAGAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGGCG
CGCCCTCCCCCGCCCGAGCCTTGGCATTCAGAGTACGGGTGAGCCCGGGCCACTTGGAGCCCGCCCTGGGGAGGGCG
CACCAGGGAGCCTGGGCGCCCGGGGCTCGGCGCGACCCCATCGGGTAGACACAGAAAGCTCCGGGACCCTTCCG
GCACCTCTGGACAGCCAGGATGCTGTGGGCCACCTCTCTCTCTCTCTCTCTGGAGGCGCTTGGGCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCGCAGCAGTGGCTTAGAAGTGTGAGGGCACTTACAGA
GGCCCTGGTCCGGGACAGCGCACCTTCCCTTGCCACTGCACCTGGCTCATCTCGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAAGCTACACTGGCTGTGGCTCAGAGCGCTTAAACCTTACGCTCCCTCTCCAGCCAC
TGATCTCCCTGTGTAGGGCACTCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTCACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCTTACAGCCAAAGTTGGCTGATGTGCTGCAGGAAG
AGTTTCAGTGCTGAACCAACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT
CTGATGAAGCAGGTGACGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGTCCTCCCTCCCTGGCTTGAATG
TCACCTTGGAGGACTTCTATGGGCTCTTCTCTCTCTCTGGATATACACACTTAGGCTCAGTCTCCACCCCGAGT
CCTGCCATTGGCTGCTGGACCCCGCATGATGGCGGGCGGCTGGCGGTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCACTGATGTGTATGACGGCCCTGGGCGCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTCTCTACCAACACAGTGTCTTGGAGCA
ATGGTGTGGCTTCAATGCCACCTTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCTGTGGCTTGGCT
CTGGCCCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGCTACAGTGAGGACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCAGAGTAGGAGGAGTGCACAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCAAGCCTGCTACTGTGCTGACCGCTGCAACTACAGACTTTCTGTGTGATGGAGCAGATGAGA
GAGCTGTGCGCATTGCAGCTTGGCAATTTCCGATGCCGGGACAGAAAGTGCCTGTATGAGACGTGGGTGTGG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGTAGTGGGACTGCTCTATGTTCTGCCCCGCAAGGTCAATACAG
CTCAGTCAATTGGCAGCCTAGTGTGGCGGCTGCTCTGGTTCATGCCCTGGGCTGCACCTGCAAGTCTATTGACA
TTGCGACCCAGGATGACGACTTTTGGCCCCCTCTCCCGATGGAGGCTGTGAGCAGCAGGCAACCC
CTTCTAGGGGCACTTATGCCAGGGGTGCCATCCACCTGTAGAAGACTTCTTACAGAGATCTTATATGATA
ACTCACTGTGGGCAACTTGGCTTCTTGTCTACAGATCTTAGCGAGATATGACTCAGAGAGTGGCCAGGCT
CCCGCGCTCTGACCGGGCGGCTGTATGCGACGCTGTAGCGGCTTCCCGCGCTGGGCTTGTCTCCCTGAA
CCAAACCCCGGCTGGGGCTTGGGCGGAGATCCAGGTCACACCTTCTGCTGCTCCCTTGAAGGCTTGAATG
GTGGCAGAGGTTCAGCCCTTGGGGCGGGCGAGTGGGTGGGCAAGATGGGAGCAGGACCCCACTGCCCATCA
AGGCTCCCTCCCATCTGTCTAGCAGCTTCCAGCCCCCACTACTGTCCCTTGAAGCCCGAGGCGCACTGCCCTCAC
TGCCCTTAGAGCCATCATATTGTGTGGAGTGGTGCAGGCGCTCGAGGGCGGCTTGTGGCCAGCTGGGCGCC
CAGGACCAACCCGAGCCCGCTTGGACCCCAACAGCAGTCTTGGCCCTTGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCGGGGGTGTGGGTAGCTGAGGCAAGAGTAGGCCACTTACTTGAAGGGGCACTGGGG
CTCTACTGAGGCTCTCTCCCTGGGGGCTCTACTCATAGTGCCACAACCTTTAGAGGTGGGTGAGCCTCCCTCC
ACCCTTCTCTCTCTGTCCCTTGGATTTTCAAGGACTTGGTGGGCTCCCGCTTGAACCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCAGAGAGTCTCTCTGTACGTGGGCTTGGCCAGACCCCAAGTCCCT
TCACCAACCACTGCTCCCAACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGAACATCCATCTTGCACAACTCTACCCAAAGTGGCTTAAAGACCGGAATGCCAATTAACATGAGA
CCCTCGACCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTGGCATCAACCAATCCCTCTCAGGGGCTC
CTCAGAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGTCTAGTAAAGTGGAGTCAAAAATAA
GGATCATACATCTC

CGGACGCGTGGGGCGGACGCGTGGGCCCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACTCTTCCCTCCCCCGC

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDAAGCSSDPFPGLTPRP
VPSLPCNVLTLEDYGVFSSPGYTHLASVSHPOQSHWLLDPHDGRRRLAVRFTALDLGFGDAVH
VYDGGPGPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCDEKCVYETWVCDGQPD CADGSDEWDSCS
YVLPKRVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQLRQDMTPGGGPGARRRQRGRMLMRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGFAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPGLPPGPTRSPPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGGATAACGTGCAGCCGAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTCGGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTGTAATTTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

007626.10501

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPFPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVAVCCLAD
GALIYRKLLFNPSGPGYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

0073293:101501

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACCTACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTGAAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTTATNATCGCACAAGCCCCTGAACCATATATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTCATACTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

00978298.101501

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCCGCGTGGGCATGGGCGCGACTGGCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCGCGCCCTTACAGGTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCGCCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGGCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAA
CATTGCCACTATTTTGAATCAGAGAATTCTTTTGGCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGGCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGCACCAAGCAAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAATTCTG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCAACGCTGCTGCGCCTGCCCCAGAAGGTGTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGAATGGGTCCCAG
CTGGCGTGTGTGACGAATTTCGAAACACCTTGGTCTTACTTCCCTAAAAATCTCCATCTACCT
GAGAGACGAGAATCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTACG
CCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCATCCACAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA
GAGGGTGGGCTTCGACGCGAGCCCTGTGCAGAAAATGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCTTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGCTGTGTGGAGCCATCCTCCTGTCTT
AATCGTCAGTGTCTGCTGCGGTTCGGGTGTGAGCTCGCCCCGTGACCCCTGAGGTCTGTC
ATGATGAGTCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAAATCATTTCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAAATTCATTCTAA

09975298.101501

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPEGGTPAERHADGLAL
ALEPALASPAGAAFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYECYRFGIS PSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
BIAGAAVSEISGFFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCGAILLVLLVLLLPFRCL
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCGTTCCAGGCCGTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGCCCCGCGCTGCGGCGGCATGGGCAACCTGCGGGGCCGACGGCCGCTGG
TCAGGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGTGGCTGCGCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTATCTTCATGGCCTTGGACTTGGCCAGTCTGGCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCAATGCC
GGTATCAGTTCCTGTGGCCGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGTGACACATCTGTGTGCTGCCTTGCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCACTGTGCGGGACGTCTTGACTTCAAACGCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGGCCCGGAGCTCGCCAACAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGTGCGCCAGACACCCTGTATTG
TGCTCTACAAGAGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACGTCCATGTGGAAG
AGGTGCCTCCAGCTGCGCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCCT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTCGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAAATTAG
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGACTCGCCTAGGGTCTCACAGTGAAGTAGGAGGAGGGGCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTGAGGGCAGGGCAGCTGTTATCGAGGTGCCCCATGGGAGTAAGGGGACGCTTCCGGGCGG
ATGACGGGCTGGGTCTATCTGTATCTGAAGCCCCTCGGAATAAAGCGGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAA

00976298.101501

<subunit 1 of 1, 377 aa, 1 stop

MEALLLGAGLLLGAYLVVYVNLVKAPFCGGMGNLRGRTAVVTGANSIGIKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHAG
ISSCGRTREAFNLLLRVNHIGPFLTHLLLPCLKACAPSRVVVVASAAHCRGLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCAAAHPGPVNSEFLRHVPGWLRPLLR
PLAWLVLRAPRGGAAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEADPEDDPQSEDEAPSSSLSTPHPEEPTVSPQYPSPQSSPDLKMTTHRIQAKVEP
EIOLG

Signal peptide:

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCTGGGGGGCAGGGGTTCCCTGCTCTGCTGCTCTCTGCTCATatgGGAGGACATGSGCTCAG
GACTCCCCGCCAGCATCTTAGTGCACCCCCCAGGACCAAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAGGCTCAGGCCAGCCACCTCCACCAATCCGCTGGTTGCTGAATGGGCAAGCCCCCTGACATGCTGCCCCAGAC
CCACACCACTCTCCGCTGATGGGACCCCTTCTGCTGCTACAGCCCCCTGCCCCGGGACATGCCCAAGATGGCCAG
GCCCTGTCCACAGACTTGGGTGTTCTACACATGTGAGGGCCAGCAACCGGCTTGCCACGCGAGTCCAGCAGAGGGGCT
CGGCTGTCTGTGGCTGTCTCTCCGGAGGATTTCCAGATCCAGCCTCGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGAATGTGGGCGCCCTGGGGCCACCCAGAGCCCAAGTCTCATGTTGGAAAGATGGGAACCCCTGC
GCCCTCCAGCCCGAAGGCACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAAGTGAACGAGGG
ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCGCGAGCCGGGTTTCCATCCAGAGGCC
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGAT
CCTGCAGAGGGCCCCAAGCTAGACCCGGGGTGTGGCTCAGCTGGAAGGTCACTGGCCCTGTGGCCCTGCCCAA
TCTTACACGGCTTGTTCAGGACCCAGACTGCCCGGGAGGGCCAGGGAGCTCCGTTGGGCAGAGGAGCTGTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCCCTCCACTGGGGCCAAAGACTACGAGTTCAAAGTGAGACCACTCCTCTGGC
CGGGCTCGAGGCCCTGACAGCAACGCTGTCTCTGAGGCTGCCGGAAAAAGTGCCCACTGCCCACTCAGGAA
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGAGCTGGGTCCACCACTGCTGAAACACCAATGGCATC
ATCCGTGGCTACCAAGCTCTGGAGCCTGGGCCAACACATCACTGCCACAGGCCAACTGGACTGTATGGTGAGCAG
ACCCAGCTGGAATCCGACCCTATGCCAGGCTCTACTGGGTGCAAGTGGGCTGCAGTCACTGGTGTGGAGCT
GGGAGGCCCAATGACACTGTCTGCTCTCTTTAGAGCAGGCCATGGAGCAGGCCACCCAGAAACCCAGTGAGCAT
GTCTCCTTGAGCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCACTTGGCACTCGGGTGTGACAT
TGGCTGTGCTCTCTGGGACCGCGGTGTGTATCCACCGCGGGCCGAGCTAGGGTGCACTGGGCCAGGTTCTG
TACAGATATACCAAGGGATGGCACTCTAAACACAGGATGGATCACAGTGAATCCAGTGGTTGGCAGACACT
GGGCTTCCACCTGTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCTCAGCAGTCCGCTGGGGCGGATGCCCGG
GACCCATGAGCTGTGCTGCTCTCTGCTCTCTGGGACTCCCGAAGCCCGGGGTGCCCTGCTTCCAGACACC
AGCATCTTTTATGCTCTCCCTATCGCTGAGCTGCCCTCCAGTACCACCAGCCAGGCCAAGTCCCAAGTCCCACT
GTCCAGCGCTCCCAACCCAGCTGTGGCCAGCTCTCCAGCCCTGTTCAGCTCAGACAGCTCAGCCGCGCAGG
GACATCTCTCTCCCGCTGTCTCTGCGCCCTGCGAGGGCTGGAGGCCAAAAGAGCAGGAGCTGCAGCAT
GCCAACAGTTCCTCCACTCTCCGGGCGAGCCACTCCTTGGAGCTCGGGCTGTGTAGATTAGAAATGAGGGTTCC
AAGAACCCTTCCCAAGCCAGAGCATGTGCCCAAGCTCTGGTTGCTGGCGGGCCCTGGGACCGAAATCTCTC
AGCTCCTCAATGAGCTGGTACTCTGTCATCTCCCTCCAGCACCCCTCTTCTCTCATGAACCTCCCAACTCAG
AGTCAACAGACCAGCCTCTCGGTGGCACACAGGCTCCTCTCTCATCTCTGCTGCCAGCAGCCCAATCCCACTC
CTTAGCCCTTCAGTCCCCCTAGCCCCAGGCTCTTCTCTCTCTGCCCCAGGCCCTTCCAGCTGCCTGTCTCC
AGCTCCTCACTGTCTATCCTGGGGGAGGATCAAGACAGCGTGTGACGTCTCCGACTCGGCTCTCTCTGCTGTCC
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCTTTCACCCCCACCACTAT
GGGTACATCAGCGTCCCAACAGGCTCAGAGTTACCGGACATGGGACGGACTGGAGGAGGGGTGGGGCCCAAGGG
GGAGTCTTGCTGTGCCCACTTCGGCCCTGGCTCACCCCCACCCAGCGAGGGCTCTTAGCCATGTTGGGGC
TCAGCTCTGAGGACAAATGCGGCGCAGCGCCAGAGCCAGCTTTGTCACTCTCCGAGGCTCCTCTCTGCTGAT
GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGATAGCTTTGGTTTCGGTCTAGAGCCCGAGGAGGCAGACTGC
TGTCTCATAGATGCTCATCACTCCTCCCCACGGGATGAGATCTCTGACCCCCCAACTCTCTCTGCCCCCTG
TGGGAGTGGAGGCCAGATCGTTTGAAGACATGGAGGTTCAGCACCCAGCGCTGGGAGGGGGATGCTCTCC
TGGCCCCCTGACTCTCAGATCTCTCTCCAGAGAAGTCAGCTCCACTGTGCTATGCCAAGGCTGGTGCTTCTCT
GTAGATTACTCTGAACCGGTCTCCCTGAGACTTCCAGAGCGGAATCAGAACCACTTCTCTGTCACCCACAAAG
ACCTGGGCTGTGGTGTGTGGGTCTTGGCTGTGTTTCTCTGCAGCTGGGCTCACTTCCCAAGCCTCAGAGAG
TATCTCCTCCACGATTTGTGAAACCAATGAAACCAAAATAGAGCAAAAGTCACTGGAGCCCTCAGGGAGCAAA
ACATCATCTCCACTGACTCTAGGCCACTGTCTTCTCTCTGTCCTCACTCCCAACAGCTGTGTTTGGC
CTGAGGAGCAGCCCTGCTGTGCTCTTCCCCACCAATTGGATCAGGAAAGTGGAGGAGCCAGAGTGGCTTT
GTGGAGGACAGAGTGGCTGTGCTGGGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCTCTCAGCTTACTCT
GGGCCCCCTCTCTAGAGAAGAGCTCAACTCTCTCCCAACTCACCATGGAAGAAATAATTATGAATGCCATCT
AGGCATCAGGGCCCTATCTCTGCTGCAAAACAAGGGTTCAAGGCTGGGTCTAGCGGAGCTGGAAGGAGGGAGG
TATGAGACCGTAGGTCAAAGCACCATCTCTGTACTGTGTGCATCTAGCTTAAGAAATTTGATACCAATAAAAT
GGTAAAAA

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGAQDSFPQIILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQFLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPRHTVSGGSLLMARAEKSDEGTVMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLSWKV
SGPAAPQSYTALFRTQTAPGGQAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDFLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSPTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLPFHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGSPASSRLSSSSSLSGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPEADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCCAGGTGTCCAGCGCCCAAGATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACACCGGAAGTACTGGTGACGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTTGGCACCATCTATGCAGAAAGAAGAGGCCAGAGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTGCAGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTGTCGTCTTCCAGGACCTGCTGTCTCCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTTCAACACGCTGACGCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGGCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCTGACAGGAGCTCCCGCCCCCATGCAAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAAG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAAGGAAGCC
 CTTTCCAGGCCCTGAGGGGACGTGATCTCGATGCTCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTGGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCCTCCCGAGCTCTCCTCTTGATGTTCCA
 GCCTGACCTAGAAGCGTTTGTGACGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTTACATCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGGACCTGCTTCTCCTCCACTCCAGACCCACCTTGCTTCTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCAATCAGCTGGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGCTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCAATTGGGCTGTGAGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCCTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCAGGACCGGCAACAGAAGTGG
 TTGCCTTTNCCATTGGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTCGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTTCTTTTCCATTATTTGTTTAAAAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGACACCACTCCGCTGAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTTGAACCTCCTGAC
 CTCAAATGAGCCTCCTGCTCAGTCTCCAAATTCGCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCCTTTAAAAAGTGAATTAAGAGTTGTTCAAGTATGCAAAACTTTGGAAG
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
 TATTTCGTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCGGGTGTCTT
 TTTACAGCAATTAATCTTGTATATACAACCTTTGTATCCTGCTTTCACCTTATCGTTCC
 ATCACTTTATTCCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

09976298.101501

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLQDAGEYWCVGVEKRGPD ESSLISLFV
FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGGKTGA EAPPLPG
TSQYGHERTSQYTGTS PHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLS AAGLIAFCSHLLLRKEAQQATETQRNEKFWSRLTAE EKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTAAGTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCAATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTTCAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCAGATCAACAGCCGGAGGTGGTGAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

0075238-101501

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
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<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD

YEADGSTNNGIFOINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY

WEAWRHHCOGKDLTEWVDGCF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCGCGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTTC
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTGTCGTCGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAACCGCGCGCTGGAAGTGTCCACAC
TCGACTCCTTGCCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTCAGTGAACGCGGCGTGAGCAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGATGGGGTCAGCCACAGGGCTTCAGTGGTCAG
GATGCTCTGACAAATCGCCTACGGTGTGGCCTTCTCAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCGCGCAG
GAAGGCCATCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTCAAGCTCCTGTG
AAGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCGCAGGTGGGTACGCACCTGAAGGAG
AGGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGTTGGCACGAGGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGTGTGTGTGGCCGCGGCTTCACACGCGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCAGTGGTGTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTGTCTGTTTGGTCTTGGGTCTCATGTATTTATTTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTATCTGTGTCGGTTTTTCTACTTGACAGACCTAAGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGGCCTTATGGCAGGAAAATA
GGTACCAGCTTGATGGAAGTCACACCCTCTGGAAAAAGAACTCTTAACCTCTCCAGCACACA
TACACATGGACTCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAAGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGTCTTTCAGGCAAGAAGAGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAAACCCAGCCTGGCCACGCCTGCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCGAGTCACCTTTCACAGCGCTGTTCTCTCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCGAGTCACCTTTCACAGCACTGTTCTCTC

<subunit 1 of 1, 351 aa, 1 stop

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEETCEKLGKLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRNRWNCSTLDSLVPFGKVVTQGTREAAFYVAISSAGVAFV
TRACSSGLEKCKGCDRTVHGVSPPGFQWSGCSDNIAYGVAFSQSFDVVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCPEVTKCWRAPFQVQGHALKEKFDGATEVEPRR
VGSRRALVPRNAQKPHTEDEDLVLYEPSCFDCEQDMRSRFLVTRGTRCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSKTHWCCFPVKRCQORLVELHTCR

Signal peptide:

N-glycosylation sites.

Wnt-1 family signature.

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGCCCTGGCTGTCTCTGGTC
ACCACAGTCTCTTTGGGCTGTGATTCTGAGTATCTTATGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCGTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTGTCATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACTGCTGACCCCGCCCACTGCCCCTGGAGCCGCGCCCAATTGCAGCATGTGCTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTITAGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

0978296.101501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTLWAVILSILLSKASTERAA
LLDGHDLRLTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR
ELRERVITQGLAEAGRGREDVRTELFRALAEAVRLQNNSCPEPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLEQGFLLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEFNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCCACGTCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGTGGAGCCTCATTTGGCCGGCCCCG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAAACCCGACCCGGCCGCCCGCCCTGGGCAAG
GCCCTCTGCCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCGCAGAGCCCCGGCCAAATACAGCATCACCTTACAGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAGCAGTACCCCCCTGTTCCGCCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCGCTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACCTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCGCCCCAGTCTCTGCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGTGGACTGCGAGGTCTC
CCTGTGCTGCTCCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGCTTAAGACCAGAGCCCCGACGCCCCCTGGGGCCCCCG
GAGCCATGGGGTGTGGGGGGCTCCTGTGCAGGCTCATGTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAAGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTGCTCCAGGAGATTGTCTTTCATCG
TCCAGGGGCTGGCTCCACAGTGGTTGCAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG
AGCCACTCTCCCGAGGGCGCATCCAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGAAGCGTCAGTGTTCATGTATTGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09/03/2016 10:50:1

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVRRLSLVSFVVRIVPSPDWFGVDSLDCGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAFVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

00978293 101501

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAAACTGAAGCTTTCTGCACTGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCTCTCATCCCCGTAAGGAGCAGAGTCCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAAC
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCTAAAGCTTGCAAAAATTT
ATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTCTTATAGAGTTGTGCGCTGGTTT
CATAGTCCAAGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTACCGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT
TAACAATAAGCATACCATTCTTTGGAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTTGTTTAAATCCTTTTGATGACATCATCCAGGGAAATTAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTT
CATTGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCTGATGAGAGAAGAATGCCAAAAA
TTAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGCAATTAAACCGGAACCTCTAGCAG
CAAAACAAAAAAAGTAGAAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGTCTGTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAATGACATCTCTGAACAGAA
GTAGAAGATGATGAAGGATGGATGTCAATGTACTTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAAAAAAGAAGAAGATAAAT
GAGAATAATGATAACCAAGACTTGCTGGAATGTGCCTACAAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGAAAAAGAAGTATTTTTGAACCTGTTGTCTGTTTTG
AAAAACAATTATCTGTGTTTTGCAAATGTGGAATGATGTAAGCAATGCTTTTGGTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

0070203.101501

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPNPFDDIIPREIKRLKKEK
PEEEVKLKPCKGTKNFSLLSFGEEAEEEEEEVN RVSQSMKGKSSSHDLLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVA EYRREKQKYEALRK
QQSKKGTSRDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWM SHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

00973298 101501

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCGCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
CCCGCTCCGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCTTGTGACGGCGTCCG
AGCCCTGGCCAGACATGTTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTCTTCTCCTTCGGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCAACTCCAGCAACTACATCTG
TCTCCTTCAAGTGGTTTTTGGAAACGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCCTTGACACACCAAGAGGCTCAAGTGGTCAACAAATATGGAAC
CCTGCAAGGAAAAAGATGCATGTGCGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA
GGAATCAGAGATGTACACCTTACCGCCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGCTACAGGTGCCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCG
ATGTACGTGACGACGCGGGAAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCGCGCGCGCCCGGGATCCCGAGCTGCCAGTGTATGGTCTTGGTTCC
CGGGAGGCGCTTTCATCTGCGGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
GAGAAAGTGGTGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGCACGGA
CGACAGCCACGCGCGCGGGAAGTGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCAGGAAATGTGACCTGTTCGGCCAGTGGCGG
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
CATTTCCAGAGTGGCACCGCTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGGTTGCCACCTGGCTGGATGCACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAACT
GAACTTCCAGAGAGACCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCAGATGACCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATACCAAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACTGGACAATGTCAATGAGCATGACTGGAAGATGTCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCACTGAAGCTCAAGGAGAAGAAGTGGC
TTTTTGGATGAGTCTGTACCACTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGACCAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAAGCTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGACCTGCAGTGCCTTTCCAGCC
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTAGCTCTCCAGCCTCAGGACAACTCTTTTTTCCCTTCTTCAAATCT
CCCACTCTTCAATGTCTCCTTGTGACTCTTCTTATGGGAGGTGACCCAGACTGCCACTGCT
CCCTGTCACTGCACCAGCTTGGCATTTACCATCCATCCTGCTCACTTGTCTCTGTCTGT
TCACATGGCCTGGAGGCTTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAGTGTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAFSSG
FGTGLFGSKPATGFTLLGGTNTGALHTKRPQVVTKYGTLLQGKQMHVGKTPIQVFLGVFPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWQGLASMYVSTREYKWLRFSEDCLYLNYYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRETMMGICPAGHATRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

007323.10504

FIGURE 92

GAGAAACAGGCCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
 GCTGTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
 AGTCAGTATGGTGGCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
 CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
 CAAGGGTGCTCTGTGGCCACAAACCACAGAGTGCAGAGGTTGGAATGAGCACCCGGGGC
 GATTCCAGCTCCTGGGGATCCCCCAAGGGGAAGTGTCTCTGGTGATCAGAGACGCGCAG
 ATGCAGGATGAGTACAGTACTTCTTTCCGGTGGAGAGAGGAAGCTATGTACATATAATTT
 CATGAACGATGGGTTCTTTCTAAAAGTAAACAGTGCTCAGCTTACGCGCAGACCCAGGACC
 ACAACACCGACCTCACTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
 GTCCGACTCCGTGTGGCCTATGCCCCAGAGACTTGTATTACGACTTTCAGTGACAAACAC
 GCCAGCCCTGGAGCCCCAGCCCCAGGGAATGTCCCATACCTGGAAGCCCAAAAGGCCAGT
 TCCTGCGGCTCTCTGTGTGCTGACAGCCAGCCCCCTGCCACTGAGCTGGGTCCTGCAG
 AACAGAGTCTCTCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
 GGTGAAGGCTGGGATTCAGGGCGCTACACCTGCCAGCGGAGAACAGGCTTGGCTCCCGAG
 AGCGAGCCCTGGACCTCTCTGTGCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
 GCAACAGGACAGTCTGGAAACCTTGGGAACGGCACGCTCTCTCCAGTCTGGAGGGCA
 AAGCCTGTGCGTGTGTGTGCACACAGCAGCCCCAGCCAGGCTGAGCTGGAGCCAGAG
 GGGGACAGGTTCTGAGCCCCCTCCAGGCTCAGACCCCGGGGTCTGGAGCTGCTCTCGGGT
 CAAGTGGAGCAGGAAGAGAGTTCACTGCCACGCTCGGCACCCACTGGGCTCCCGAGCAGT
 CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCAACGGAG
 CGTTTCTGGGAATCGGCATCAGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG
 ATTCACCGAAGAGACGGATCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
 GATCTCTGGATTACATCAATGTGGTCCCGACGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
 AAGCCACACCAACACGTCTCCGAGCCCTCTCCACAGGTGCTCTCTCCCGAGAATCAAG
 AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAATCATCCACTCAAGC
 CCCAGAATCCCAGGAGAGCCAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
 GACCCAGGCTGAGGCCCGGATGCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTT
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
 GTTGAAGATAACAGAGTGCAAAAGTTTCTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCT
 CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCAGCCCTGTAATC
 CCAGACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGGTTGCAGAACCGACCTG
 GCCAACTTGGTGAACCCCGTCTCTACTAAAAATACAAAATTAGCTGGGCATGGTGGCAGG
 CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
 AGGTTGCACTGAGCCAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
 TCTCAAAAAAAAATCTCCAAATGGGTTGGGTGTCTGTAAATCCAGCACTTTGGGAGGCTA
 AGGTGGGTGGATTGCTTGAGCCAGGAGTTCGAGACAGCCTGGGCAACATGGTGAACCC
 ATCTCTACAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCTCTGTAGTCCGAGCT
 CAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAATGAGGCTGAGAG
 TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCAAGGATGAGACAGGAGTCCG
 TACAAGATCAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAACCAACCA
 ATCCCAACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTCTCTACTGCTACACTCT
 GACAGCCCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
 AAAGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAAATGAAGCAAGAAATAACCATAAAA
 GTGGGCAACAGCAGCTTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTCTCTT
 TACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK
AVTETTTGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCNSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSTTPRPQDHNTDLTCHVDFSRKGVSQARTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLLCAADSQPPATLSWVLQNRVLSSHPWGPRL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDSVQYPPENLRVMVSQANRTVLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSFSPQSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPPEP
KSSTQAPESQESQEBELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGCTGTATTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGCTCTTGGAGCAACAGAAAACCTCTCAAAACAAGA
AAGTCAAGCAGCCAGGTGCGATCTCATTGGAGAGTGAAGCGTGGCTGGGTGTGGAAACCAATT
TTTGTACCAGAGGAAATGAATACGACTAGTCAATCAGCTCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAGAACAAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAACTCTGAGTCTGA
GTTTGTGCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTCTGTTGAACCAACAACAGGAGTCAATGAAGATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTTGGGTAATCATTTCAAGCCAAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACCTTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCCTCGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT
GATTCCGAAACATTGTGACATTATTACTAATCAAGAACTCAAGAAAGAAATAGTTATATTTAA
AAAGAAAGTGGATTTTGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTTAAAAACCAT
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTTCATTAAAGTCCAG
GTGGAAGATGTTGATGAGCCTCTCTTTTCTCCTTCCATATTATGATTTTGAAGTTTGTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGAGCCAGACAATAGGAAAT
CTCCTATCAGGTATCTATTACTAGGAGCAAGTGTTCATATCAATGATAATGGTACAATC
ACTCAAGTAACTACTCGGATCGTGAATCAGTGCCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTCATCATAGATAATCAAG
ATAACACAGCTGTCATTTTGACTAATAGAACTGTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAGTACAAACACCCCTTAC
CATCCATGTCGTGACTGTGGTGACAGTGGGAGCACACAGACTCGGAGTCAACAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTTGCTATTCTCATTGCAATTATGATCATA
TTTGGGTTTATTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTTCTGT
GAAAAGTGAAGATTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTTGGCCCCGA
CAGTCCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATCATGATCCGTGTG
CCGCTCCTTTGATGTCCTCCAGACCTACGCTTTTGGGGGAACAGGGTCTATTAGCTGGATCC
CTGAGTCTCTTAGAATCAGCAGTCTCTGATCAGGATGAAGCATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTACCATCAAATTTTAAAGTGCTAATGTGATTCGAACCCAATGGTGTAGTCTTAA
AGATTTTTTGCCCTTGGCTCATGGCGGGAAAGCCCTAGTCTATTGGAGTTTCTCGATTTC
CTGGAGTAAATACTCCATGGTTATTTAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACAGGATTTTGAAGTAAATTAATG
TAGGAAGATATTAAGAGTATGAGAGGACACAAGATGTAGTCGATCTTATGCGATTATAT
CAATTATTACTTAGGAAAGAGTAAAAATACCAACGAGAAAAATTTAAGGAGCAAAATTTG
CAAGTCAATAGAAATGTACAAATCGAGATAACATTTACATTTCTCATGATTGACATGA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTTAT
TTAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSRLRVKRGWVWVQFFVPEEMNTTSHH
IGQLRSDLNDGNNSFYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARL
LYSLAQGPYFVSVEPTTGVIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSTIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVVFVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNLDREISA
WYNSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETVCENAGSGQVIQTISAVDR
DESIEEHFYFNLSEDTNNSFTIIDNQDNTAVILTNRTGFNLQEEVPVYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAI FRKFILEKLEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTC AAGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTTNTGGAACAACAAGTGTATTAATTAAACTTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAAGTTTATACCGCTTGACTGTTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

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T05T07-82287660

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACTTCTCCGCGGGG
CCAGCCACCTTCCGGAGTCCGGGTTCGCCACTTGCAAACTCTCCGGCTTCTGCACCTTGCCA
CCCCTGAGCCAGCGCGGGGCCCGGAGCGAGTCAATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCTCGGATGGATCGGCGCCATCGTCAGCATGCTTCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCCCGACAAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCCTCGGTGTCGACAGGCAACCGGCGAGATCCAGTGCAAAAGTCTTTGACTCCTTGCTGAAT
CTGACGAGCACATTTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCTCTCTGGGAGTGAT
AGCAATCTTTGTGGCCACCCTTGGCATGAAGTGTATGAAGTGCTTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCTATTTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAGAATTTCTATGACCCCTATGACCCAGT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGTCGCCGAAACCAACCTCTTACCCAAACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAGACTACGTGTGACACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC
CTTAGAATTTTGGGTATGTTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAA
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCTCA
ATATAGGAGGGGAAGATTTTCCATTGTTATTACTGCTTCCCATTTAGATTAATCATACTCAAA
GGGGGAAGGGGTGCTCTCTTAAATATATATAGATATGTATATACATGTTTCTTCTATTTAAA
ATAGACAGTAAAATACTATTCTCATTATGTTGATAGTACTAGCATACTTAAATATCTCTAAAT
AGGTAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTCTTTTTCGTC
TTATATACATATGTAACAGTCAAAATCATTTACTCTTCTTCAATGCTTTGGGTGCGCTTTG
CCACAAGACCTAGCCCTAATTACCAAGGATGAATCTTTCAATCTTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCACTCGTATTAAAGCCCTTAT
TTGTTTTGTTTTCAATTGGTCTCTATCTCTGAATCTAACACATTTTCATAGCTACATTTTA
GTTTCTAAAGCCAAGAGAATTTATTACAAATCAGAACCTTTGGAGGCAAACTCTTCTGCA
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAAATCCCTGTAATCTGACCCATAGCACT
CTTGTTTGTCTTTGAAAATATTGTCCTCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTATTTGATTGAATTTTAAAGCTACTTATTCATGATTTTATATCCCCCTAAACT
ACCTTTTTGTTCCCCATTCTTAATGTATTGTTTTCCCAAGTGTAATTTATCATGCGTTTTTA
TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTTGAGATAATGATACCTTAACCAAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGTCT
CAGCTGGCTGAGACACTGAAGAAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATT
CACTGCCCTTCTCTCTACCAAGTCTATTCCACTGAACAAACCTACACACATACCTTATCAT
GTGGTTCAGTGCCCTTCCCTCTCTTACCAGTCTATTTCCTGACGAACAAACCTACGCAATAC
CTTCATGTGGCTCAGTGCCCTTCTCTCTTACCAGTCTATTTCATTCTTTTTCAGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAACTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGACAGAGATGTAAATGGAAAGGGTGTGGCAGCTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGTCTCAATCACCGTCTGTGTTTGAAGCAAGGCATTTGGCTGCTGTAA
GCTTATTTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG
TTGTGGGATCCAGTGAGATGAATACATGTAAAGTGGTGTGTAATTTAAAAGTGCTAT
ACTAAGGGAAGAAATTGAGGAATTAACGCATACGTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AF~~L~~GWIGAI~~V~~STALPQWRIYSYAGDNIVTAQAMYBGLWMSCV~~S~~QSTGQI
QCKVFD~~S~~LLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMT~~P~~VNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTT~~S~~YPTPRPYPKPAPSSGKD~~Y~~V

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCTGGGATGGATCGGC
GCCATNTCACTGCGCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCAGCCCATGTACAGGGGGCTGTGGATGTCTCNGCGTGTGCGAGACACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGTTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCTATTGGGGGC
GCGATATTTCTTCTTGCAAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAA
NNTTCAACANTTCTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GCTCTCTTCTTACTGGCTGGGCTGCTGCTTCTCTCTGCGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNITGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCAITGGGGGCGGATATTTCTTCTTGAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCCTATGACCGA

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GGGCCCCGACCATTATCCAACCGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCCG
CATCNTCAGACTCCCTGCCCCATGGAGATTNNCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNCAGCACATTGCAGCAACCCNTGCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCCTTGGCATGAAGTGATGAAGT
GCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTATTGGGGGCGGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCATGACCCCACTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

FIGURE 102

ATTCTCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCAGGCCATTACCGAGGGGCTTGGATGTCNT
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTCTGTCCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

09978298.101501

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGT CATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCCCTGCGAACC

09973298 101501

FIGURE 105

TCATAGGGGGCGCGATATTTTTCCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAAATNTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCTCTG

09978298.101501

FIGURE 106

TTCTCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCAGGCATGTACGAGGGGCTGTGGAATGTCTGCGTGTG
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCAT
TGCAAGCAACNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCATATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

0076298-101501

FIGURE 108

GCGTGCCGTCAGCTCGCGGGGACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCCGTGCCCCG
ACCGGTCCCCGCCCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCGCAGCAGCAGCTCAAATTCGAGGTCCCTTACCAGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
CAGCACCACGATAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAGTAAACCAAGTT
TATGTTTCACTCTATGTTTGTCCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCATGATGTAGTAATAATAATAAATATATATCCACAACCTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAAGGGCTACGGGAGGAGAAACAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC
CCCAACTGGGAAGGAAGAACGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTGTCTCTTA
TCGTTGGTGAATTAATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAGAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTAACCCCTCCCTGCACACACATACAC
AGATACACACACAAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAAGGAAACCATGAGTAATGCCACAAT
GGCATATTTGTAATGTCAATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
TCTTAAAAATGACACCCCTTCTCGCCTGTTGGTGTGCGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCAGGTGAGCTCCACAGTAGTCCCCACGTGGGCCCACTCCCGGCCAGGCTG
CTTCCGCTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTCTACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCATCTCATGTTTCTTATTGTCAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACCTCTGTTGGGTGAACCTGTTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATCTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGGAAGAGAAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAGAAAAATTATAATAAGCCCCAAAATTAGAAAA

<subunit 1 of 1, 243 aa, 1 stop

MAKVEQVLSLEPQHELFKFRGPFTDVVTTNLKLGNPTRDNVCFVKVTTAPRRYCVRPNSGIID
AGASINVSVMLQPFYDYPNEKSKHKFMVQSMFAPTDTSDEAVWKEAKPEDLMDSKLRVFE
LPAENDKPHDVEINKIISTTASTKTETPIVSKLSLSSLLDTEVKKVMEECKRLQGEVQRLREE
NKOFKEEDGLMRKTVOSNSPISALAPTKEEGLSTRLLALVVLFFIVGVIIGKIAL

Transmembrane domain:

amino acids 224-239

amino acids 68-71

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

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FIGURE 111

TATTGTAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCN TTCCTCGCCTGTTGGTGCTGGCCN TTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCC GGCCCAGGCTGCTTT
CCGTGTCCTTCAGTTCGTGCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAC TGTTATT CAGAGATGTTTAAATGCATATTTA
ACTTATTTAATGTATTT CATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGTGAACTGGTATTGCTGCTGGAGGGCTG

09973293: 201501
T05107: 0623/060

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATINTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

09978298.101501

FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTCCGGTNTTCAGTTCCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGT
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

09978298-101501

FIGURE 114

TGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGCCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTCATCTCATGTTTTCTTATTGTACAAGAGTACAGTTAA
TGCTGCGTGC

00978293-101501

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAAATGACAAGGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG
TTTAATGCATATTTAANTTTAATTAATGTATTTCATNTCATGTTTTCTTATTGTACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

00973293-101501

FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCAGGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTGGAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTCATCTCATGTTTTT
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAAGTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

00978293-101501

FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCGGCCCTTGGCGGGGCGGCCCTCGGGCTCAGGCTGGCTGAGA
GGCTCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAAACAGCCTCGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAAGTGCCA
TGATCATGTTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAATAATATGCTGCTTTGGTTGATATTTTTACC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGATTTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCCTATGAGACTGTCTTTGAGAATGGCACC CGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAATATCACCACAAGGGAG
TATCTGTTAGGAGAAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTTGACAAA
AGGTTCTTAACCAATTTCCCTTTAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCCAGTGTGTTGATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACCTCGAGGTTCTAAGAGAGAGCAGGAGAGAAGCTAGTGGTGGTGACC AAAAGAGGGGTAC
CAGAGAGCATCTCGCAGGAGAGCGAAGGGTGGGAGAAGAAAGAAAATCTGGCCGGGCTC
AGAGGATTGCCGAAGGGAGGGCCTTCTTTCACTGAGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGAATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAA
TGCCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGCAGTGTGTCGACGAATCCAATGATCTCCTTTACCAATACGCGATGCTGAGTC
GGGCTCCACCCGGTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAAATTGGAAGC
GCAAAATCATTTGCGGTCTACTCAGGGCACCAAGTGGTGGATGTCCACGGGGTTCAAGAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCCTAAAAATACGCCAGATTGCGCTCTGGATTCAAGG
GAACGATGCCAATTGTGCTTACGGCTTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACAGGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAATGTGAAATGATGATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTTACACACAGTTTGTACTA
CTCTGAGATGGATCCATTCACTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTAGTTTATGTTTTTTGAAGAATTACAAATCAGAGAAGAAAAGCAAGCATTATAAA
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTATTTAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAGCTGAGACATT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAATATGGACTTTTCATGTATGATAGG
AAGACACTTCACAAATATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTGGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
CTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGCTCTTCTTCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDSNDLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKIIAVISG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACCTTAGCAGCTTATTAGTGTCGGAATCTGATTCGGCAGAG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCGTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAAATGCAGTAATGTGGAC
TGCCCAACCAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCTGTGTCTAATGACCCGTGACAAACCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCTGGTGTGTTGAAGTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAACTTTGGATATGTGCATCAGTGGTTTATGCCAAATTTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGTTGCACTTCCTATGGAAGTAGACATATTCCGCCCTTGTCTTAAAGGTCTCTGATCACTT
ATATCTGGAACCAAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTGTAACCTCGGCTCCGCTGACAG
TACAGTCCAGTTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCTACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCTTCTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGTCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTTCAGTTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGAGGAGCCCTCGTAAAGTTGTAAGCAAGCAGACTGTTCTATA
TTTGAAACTGTTTGTGTTAAAGAAAGCAGTGTCTCACTGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

00973298.101501

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECSTCGGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLFPVSNPDNPCLKQC
AKGTTLVVELAPKVLDTGRCTYESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHRLVLKGPDLHLYLETKTLQGTKGENSLSSSTGTFL
VDNSSVDFQKFPDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQLRYRVVLCIDHRGMHTGGCSPKTKPHIKEBECIVPTPCYKPK
EKLFPVEAKLPWFKQAQELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAAC TCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC
AGATGG CAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTCTGTGGGGCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCCGSCCTCAT
GCACGGGAAGACTGTGTGATCACCGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCGGGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCGCGCGAGTGGCGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGA CTCTCAAAGTT CAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTT
TACCAGGGAACTAGCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTGTCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGTTCAAACCACTCTTC
AATTTGGTGT CATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCCAGACTTCCATTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGT CAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCTGCTAAGAGGTACATGTGGGTATTTTGAGTTACTGAAAAATATATTT
TGGGATAAGAGAATTT CAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGT CAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAATTAATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

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FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEAAAGQLRRELQAEECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLGLLKSSAPSR
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGNTVTVNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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105101.8028660

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAATTATCTGCCTGGCTT

00973498-101501

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGCTCCCGGAGCCAGCC
CTTTCCTAACCCAAACCAACCTAGCCAGTCCCAGCCGCCAGCGCTGTCCCTGTACGGAC
CCAGCGTTACCAATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACCTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAATGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGCATAGCCCC
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACATATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCGGGCATTCTGCTCCGATATGGGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTCTCTT
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCTGGAAAACTCAAGCAATTCTG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT
ACAGCCCAGGAGAGCAAGCCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAACTTG
AAAAACAGTTTTGTAAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA
TATTTTCATAATTCTATGTGATTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRCFSQ
MLHPIFEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNRYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYL GAMTNFDVTYNW IQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPPESSFQKLAPSEYRYTLRLDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTA

09978299.101501

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGTGTTGCGCCGCGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGAGCCCAGCCCTTCTTAACCC
AACCCAACCTAGCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGTTTTAGTCAAG
ATGTGGCATCCAATTTTTGAGGANGCTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

0976298.101501

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGAATACCCCTGAATCCCCTTGTA^{CT}CTCCAGAGTACCTCAT
CCACGCTTCTTCTGTGTCATGTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTATGAGTGGCCCAGGA
CTCTATGACCCACAACCATCATGAATGCAGATATTTCTAGCATATTTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTGCACCTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTGTGTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTTCATGGGTTTCCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGC^{TT}TAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTGTCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATGTATAACCATCTGCTGTTCTTTTAGT
GCAATACAATAAACTCTGAAATTAAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

00976248.101501

FIGURE 130

ATTATAGCATTGTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCCCTG
AATCCCCCTTGTA CTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

00973298.101501

FIGURE 131

CGGACGCGTGGGGGAAACCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCG
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGCTCTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGAGGCTGTTTTCAATTGTG
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTGCTGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATCCACTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG

09973298.101501

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRACQLTYPLHTYP
KEEELYACQRGCRIFLSICQFVDDGIDLNRKLECESEACTEAYSQSDEQYACHLGCCQNQLPFA
ELRQEQLM SLM PKMHL LFP LTLVRSFWS DMMSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

0076208-101501

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG
TGAACTGAGACAAGAACAACCTTATGTCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978298.101501

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGGAACAAGATGGCGGCCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTGAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTGAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTTCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCTTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

00976296-101501

FIGURE 135

GCAGAGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCCTGGGAGGCGGCCCGGAGGT
GGGGCGCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGCGCACGGCCCCGACACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG
GGGATTCCTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGTAGATTTAATACTACAGGCTTTTCCCAAGACTACAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAAACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCACTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACCTGTTTAAAGCCAC
AGACAATTAAGAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTGAGTGAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAAAAAATGTTACTTCTGGAATACTTCATGAAATCAAGTCATTTCCTTTG
CATTTTGATGAGAAATCATTTTTTGCTGGGGATAAAAAAGAAGCACAAACTAAAGGAGGA
CTTTCGACTGCATTTTGAAGAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACCTGCTCTGAAGATCTTATTTTCTGAG
AAATGTATAGCAAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACGACAGAAGA
AATAGTATCATTATTCAACGCATTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAACT
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTTGTTTAAAGTAAACACATTTT
AAAAAATGTGTTAAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLD DCTCDVETIDRFNNYRLF
PRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALS KVL PFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGSPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

00975298 101501

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCATACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTGTATGGAATTTTGACTGAAGGAGAAAGGTCCAAGAAGG
CTTAAGAACTTGATTTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNNTTACTGAAAATAAAATTCAGGATGAGGNAACAAAA
TGTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGGAATTCA
TTTTTTTGCTG

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGCGAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACTCGGATGAACATCACCCAGCCTATTCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCCTCCAAGCCTGGGAGTAACATATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCCTGGGATATGTGCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCTTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCTTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGAGGCTAAGACAGGAGACTCTCACTTCAACCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCGCTGTAATCCCAACATTTTGGGAGGCCAACGAGGAGGATTGCTTGAGGCTTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

00975298 101501

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

00978298.101501

FIGURE 140

CACAGTCCCCACCATCACTCNCCTCCATTCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

00978298-101501

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA
 AATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGTTTTTCT
 ACGCATTTGATTCATGTTTTGCTCAGAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACAGGGGGAGTACGAGAGCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGTAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAAGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGAG
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTGGCTTATGCTGATCCTTGT
 GGTGCTGCCACTGTTTCGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
 TGGTCTCCAGACACCTTGAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAAG
 GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
 CTCATAGGTTTTCGGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGAACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCCAGATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACCTCAAGCCCAATGCCGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGGAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTCAGCAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

00978299.101511

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
TVYYSVEYQGEYESLYTSHIWIPSSWSCSLTEGPECVTDITATVPYNLRVRATLGQSQTSAW
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEHHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFAFVGFMILIV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

00073293-101501

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACATTGAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAAGTGAAGTCTACCAATGACAGACTTTCACAATGGTCTTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACGAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGAAATGGCTTNCACCTGGTATTGAGCTGGAGGACCTGG
GGCCCCGATTGTAGTTCCTTGTGGCCATTAGGAGAGGGCGAAGCCCTTGGCGGCGCAAGGG
GTTNCGAAGACCCCTTGCGCCCTGGGGTATCTCTCGAGAAAAGGAGGCCCAATATGACCC
ACATACTCAATATGGAGCAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLTYNTRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE
TVTWILIDRALNITSLQMHSRLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGGCGCTGTGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCCGCGCGAGCCTC
 GTTCGTGTCCCGCCCTCGCTCCTCGAGCTACTGCTCAGAAACGCTGGGGGCGCCACCTTGGCAGACTAA CGAA
 GCAGCTCCCTTCCCAACCCAACTGCGAGTCTAATTTTTGAGCGCTTTGGCTGCATTTCTTCCAGGTTAGGGGAGC
 CGCAGAGCGGGAGGCTCGCGTATTCTGCGAGTACAGCACCACTGCGCCCCGGAGCGCTCGGTGCTCAGGGCCCTT
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGCGGCTGCGAGGCGGGCGCTCCGGTTTGGCT
 CACCTCTCCCGAGAACTTCACACTGGAGAGCAAAAGAGGTGGAAGGCTGTTCTTGGAGATTCTTCTGGGGAA
 ATCCTGAGGTCTTCATTGTGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACACAGTCTGTTTCATGCTAGA
 GCAATTTCCAGCCATGTTGGTTTCCCAATGCCATTTATTGGAGAACTTTTGGAAAAATACATGGATGAGATGGT
 GAGTGGTGATAGCCAAACAAAGAGGGGAAAGGGCCATCACAGACATGACATGCGAGGTATTTTTGGACCTTCAT
 AATAAATACGAAGTTCAGGTGTATCCAAAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCGAAGTCTCGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGTCTTCATCAATCAATGGACAGAAT
 TTTGGGAGCACACTGGGGGAAGATATAGGCCCCCGACGTTTCATGTACAACCTGGTGTATGATGAAGTGAAGACATTT
 AGCTACCCCATATGAACATGAATGCAACCCCATATTGTCCTTCAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTCTGTGGGCAACTAGTAAACGAAATCGGTTTGTGCCATTAAATTTGTGTCATAACATGAACATCTGGGGGAG
 ATATGGCCCAAGCTGTCTACCTGGTGTGCAATTAATCCCAAGGGGAACTGGTGGGGCCATGCCCTTACAAA
 CATGGGGGCGCTGTTCTGCTTGCACCTAGTTTGGAGGGGGCTGTAGAGAAAACTGTGCTACAAAGAGGG
 TCAGACAGGTATTATCCCGCTCGAGAGAGGAAACAAATGAAATAGAACGACAGCAGTCAACAGTCCATGACACC
 CATGTCCGGACAAAGTATGATGATAGTAGCAGAAATGAAGTCATAAGCGCAGAGCAATGTCCCAATTTGTTTCT
 TGTGAAGTAAAGTTAAGAGATCAGTGCAGAGGAAACAACTGCAATAGGTACGAATGCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGGTACATTTAAGATGCAATCGAGCATCTGTAGAGCTGCAATTCATTTATGGT
 ATAAATAGCAATATGGTGGCTGGGTAGATATCTAGACAGGAGGAAAGCAATTTTCATCAAGTCCAATAGA
 AATGGTATCTCAAACAATTTGGCAATATCAGTCTGCTAATTTCTTCAGAGTCTCTAAAGTAAACAGTTTCAGGCTGTG
 ACTTGTGAACCACTCTGGAACAGCTCTGCTCAATTTCAAGCCTGCTTCACATGGCCAGAGTATACCTGCTCCT
 CGTAACTCTATGCAAGCAATCCACATTTATGCTCGTGAATTTGGAACCTCGAGTTTATTCTGATCTGCTCCAGTATC
 TCGAGAGCAGCAGTATGCTGGAGTGGTTTCGAAATCAAGGTGTTATGTTGATGTAATGCCTGGGACAAAAGA
 AAGACCTCAGTCTGCTCTTTTCAAGATGGAATCTTTCAGAAAGTTTACAGAACTCTCCAGGAGGAAAGGCATT
 AGAGTGTGTTGCTGTTGTGGAACCTGAATACTTGAAGAGGACCAATAAGATCTTCCCAATAGCAATATTTCTC
 ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCACTATTTCAGCCCCAAAAGGTGCAAAATGCATA
 TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTTAGCTTTAGCAGTTATTTCACAGTTAATTCATAGTCATGATT
 TTTTAGAAATCCTGTGTTTAAATATTGCTATATTTTCTTAGCAGTTATTTCACAGTTAATTCATAGTCATGATT
 GTTCTACGTTTCATATATTATATGGTCTTTGTATATGCCACTAATAAATGAATCAAACTGAAAGAACTTCATCACTTTTCCCC
 GCCTTCAGAAAATCATCTAGTGCAATTTAAAAATAATCGACTCAAACTGAAAGTGAATGAAAGTCAAGTGGTGGT
 AGTTCAATGCTATGCCATTACCACTCCAAATAATCTCAATAAATTTCCACTTAATACTGAAAGTCTTTTTC
 TGTAAATTTAGGCATATAGAATATTAAATTTCTGATATTGCATCTCTATTTTATATAAAATATACCTTTAATATC
 CAATGAATCTGTTAAAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAAGTGGTGGT
 ATGAAAACATCTCTAGTGATCATGTAGTAAATGTAGGTTAAGCATGGACAGCAGCAGAGCTTTCTATGTACTGTTA
 AAATGAGGTCAATATTTCTTTGTATCTGGCAATATCTCCTGAGGCGCAGGAAGTATAATAGCAAAAGTT
 GAAACAAAGTGAACATATGATTTACATTAACATTGCCATGATTTTTTTTAAATGGTAAATGACCTTGTATATAA
 ATATGCCATATCATGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGATTTGTGCTTTGATACATAA
 AATCTGTAAGTGTAGTTTGGTAAATTTTTTCTGCTGGTGATTTACATATTAATTTTTTCTGCTGGTGGGA
 TAAACATTAATAATCATGTTTCAAAAAA

0007306.101501

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTLVFMARAIPAMVVPNATLLEKLEKLYMDEDEGEWWIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPA SLPSIGQNLGAHW
GRYRPPTFFHVQS WYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC
HNMNIWGQIWP KAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY
YPPREEETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR
YECFAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDMPVDK RKTYIASFQNGIFSES LQNPPGGKA FRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCACGCGCG
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGACGAGCACTGCCTGACCCCCAAGCTGC
AGAGCACCAGCGCTTCATCAAGTGGTACAACGCCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTT
TTTTTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAGGGCTTCAGATGGGAGAGCCACTCTCTTGTGCT
CCAGACTTCATCAAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGCTTTCTCTTTTAA
AAAAATGCTTTTTTGTATTGTTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA
GGAACAATGAGCTTGGTGGACACATTTATTGCAGTGTTGCTCCATTCTAGCTTTGGGAAGC
TTCCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTACACACCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCGTTGACAAAGGAA
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCCATGTAATTCCTCAATGTTAAACAGTGCAGTCTCTTTGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCTTAAGAACGCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACATTAGCAT
TGCAATGAGGTTTCATATTCTTTCTAAGATGGAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAAAA

00978203-101501

FIGURE 149

MSLLPRRAPPVSMRLLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKNVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

00978293-101501

FIGURE 150

GCCCAGGGAGTCTGCTATGGCTTCCTTTGTTGTTCACCCCGGTCTGCGCTCATGTTAAACTCCAATGTCCTCTGTG
 GTTAACTGCTCTTGCCATCAAGTTTCACCCCTCATTTGACAGCCAGCACAGTATTCAGTTGTGCAACACAAATTTATGG
 CAAAATCCGGGGCCTAAGAACCCGTTACCCATGAGATCTTTGGGTCCAGTGGAGCAGTACTTTAGGGGTCCCCCTA
 TGCCTCACCCCCACTTGGAGAGGGCGGTTTCAGCCCCCAGAACCCCGTCTCCCTGGACTGGCATCCGAAATAC
 TACTCAGTTTGTCTGTGTGTCGCCCCAGCACCTTGGATGAGAGATCCTTACTGCATGACATGCTGCGCCATCTGGTT
 TACCCCAATTTGGATACCTTTGTATGACCTATGTTTCAAGATCAAAATGAAGCTGCTCTTAACTTAAAGTATCAGT
 GCCCAGGAAGATGGAGCCACACAAAGAAAAACGCAGATGATATAACAGGATTAATGACCGTGGTGAAGACGAAGA
 TATTATGATCAGAACAGTAAGAAAGCCGTCATGGTCTATATCCATGCGGGGATCTTACATCGAGGGCACCGGCAA
 CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCAITTAACATCGCTTGGGAATAC
 AGGGTTTTTAAAGTACCGGTGACCGAGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTCGCGGTG
 GATTGAGGAGAATTTGGGAGCTTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGCTGGGGCTCAG
 CTGTGTCAAGCTGTTGACCCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTTAGAGCGGCGACCGC
 GGCACCTACCCAGCATGTTAGATGTCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
 GGCCACCTACCCATAGCCTTCGGGCGGTGATCGACGGCGAGCTCATCCAGACGACCCCCAGATCCTGATGGA
 GCAAGCGGAGTTCTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCTGAAGTTCTGTGAGCGGCAT
 CGTGATTAACAGGAGCGGTGTGACGCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG
 CTACCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGACTGGGCGGATTAAGGAAAAACC
 GGAGACGGCGCGGAAAACCTTGGTGGCTCTCTTTACTGACCAACAGTGGGTGGCCCCCGCGTGGCGCCGACCT
 GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCTCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG
 GGCAGATTGGGCGCATGGTGATGAGTCCCTATGTCTTCGGCATCCCCATGATCGGTCCACCGAGCTCTTCAG
 TTGTAACTTTTCAAGAACGAGTCTATGCTCAGCGCGGTGGTCTGACCTACTTGGACGAACCTTCGCGAAAACCTGG
 TGATCCAAATCAACAGTTCTCAGGATACCAAGTTTCATTCACACAAAAACCAACCGCTTTGAAGAAAGTGGCGTG
 GTCCAAAGTATAATCCCAAAGACAGCTCTATCTGCATATTGGCTTGAACCCAGAGTGAGAGATCACTACCGGGC
 AACGAAAGTGGCTTTCTGGTTGGAACCTGTTCTCTATTGACAACTTGAACGAGATATTCCAGTATGTTTCAAC
 AACCAAAAGTCCCTCCACAGACATGACATCATTTCCCTATGGCACCCCGCGCATTTCCCGCAAGATATTGGCC
 AACCAAAAGCGCTCCCACTCTCTGCGCAACAACTCAAGAACCTTCAAAAAACGGGCTGGA
 GGACAGAGTGTCTCTATTGAACCAACAGAGATTATCCACCGAATTAAGTGTCCACATTGCGCTGGGGCTCAG
 GCTCCCTCTCTCAACATCTTAGCTTTTGGGCGCTGTACTACAAAAAGGACAAGAGCGCATGAGATCATGCTGCG
 CGCCCCAGTCCCCAGAGAAACACCAAAATGATATCCTTCATATCCAGACGAAGAGATCATGTCTCTGCAGAT
 GAAGCGATCGAACACGATCCAGAGTGTGAGTCTGCTGACGSCACACGACACTGAGCTCACCTGCGCCGCGAGA
 CTACACCTCAGCGTCCGCGGCTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCACAA
 CACACTGACGGGATGCGACCTTTGACACACTTTTAAACACTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
 CGGACATTCACCACTAGAGATAGCTTTTGGCCCTATTTCCCTTCTCTATCCCTCTCCCTCCTCGCTCAGCAACAT
 AGAAGAGGGAGGAAAGAGAGAAAGGAGAGAGAGAGAGAAAGTCTCCAGACCGAGAAATGTTTTTGTCCCAT
 GACTTAAGACAAAAATGCAAAAAGGCAGTCACTCCATCCCGGACAGCCCTTATCGTTGGTGTTTTTCCAGTATTAC
 AAGATCAACTTCTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAACTGTCTTTAAGATCTCTACCA
 CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCACAGCTCATGGAAGCAGCT
 GACACTTCTGAAACTCAGCCAAAGGACATTTGATATTTTAAATTAACATGGAGGTTTAAACATTTCTTTCTGTGC
 CACACAATGGATGGCTCTCTTAAAGTGAAGAAAGAGTCAATGAGATTTTCCCGACACATGGAGCTGTAATCCAG
 AGAGAAGGAAACGTAGAAATTTATATTAAGAAGATGGACTGTGACGCAAAATCTGTACGGTTCTGTGCAAGAG
 GTGTTTTCCAGCCTGAACATATATTTAAGAGACTTTGT

09976298 101501

FIGURE 151

MLNSNVLLWLTALAIFKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPPEPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFNTANLDTLMTYVQDQN
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG
NQGEGLKFVDGIVDNEGDVTPNDFDFSNSFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPWADSAHGDEVPPYV
FGIPMIGPTBELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTELESVTI AVG
ASLLFLNILAFAALYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCLPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGCGCACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTGTTGGGGTCTGGGCGAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTCGAGTACTTGAACCGGGAGCACTCGCTGTGAAAGCC
CTACCAGGTTGTGGGCAACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCCTTACCCAGATATGCAAAAGTAAACAGGGTGCCCTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCC
CTGTGTTTGGAAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTGGTGATTTCGCTACGTCAAAGAGGCATTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCTGCC
CCGCGGCTACTACTTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCTTGAAGTTGTTTGAACCTGACAGTGGAGAGAACCCAGAAAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCATGCGCGCC
CCTGAGTGGCCCTGGCCCTTCTCCATCGTCTTTTCTCCCTGGTGTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCAGCTG
GCCTGAGCATGCGCCTGGAGAGTGTTCTTGTCTTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTGAATGACGGGACCCCGCATTTCCCATGGTTGTGATGGGGACATCTAACT
CTGCTGTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCCTTCCCTGCAGTCC
TTCATATGTTGGGAGCAGAGGTGTGAAGAGAATTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTGT
AATCCACAAGAATTTAAAACTGGTAACACCACAGGCTTCTGACCATCCATTGTTGGGTT
TTGCATTTGACCAACCCCTCTGCCTACCTGAGGAGCTTTCTTTGGAACACAGGATGGAACCT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTTCATTGTCTCTCTGTGTGCAACCTGAGCTG
GGAAGGCATTGGATGCGCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGTTTAC
TGGCCTTCATTAGGTGGCCCTAGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACAGCTCCAGGTTTGTATCAAACCAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT
TACGATTTTGTGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTCTCTTACACCTT
GGGCTTGGATATTGCCCAGAGAAGAAATTTGGCTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAACTCTGAGAGCAACAGACCCCTCATCATCTGTGCGCTGGAAGAGTT
CACTGTCTATTGAGCAGCAGCAGCCTGAGTGCTGGCCTCTGTCAACCCCTATTCCACTGCGCTTA
TTTGACAAGGGGTACATGCTGCTCACTTACTGCGCTGGGATTAATCAGTTACAGGCAG
AGTCTCCTTGGAGGGGCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATACCCGATGGAACCAAAAAAAGGGCGGCCGCGACTCTAGAGTGC
ACCTGCGATAGGATAACAGGGTAATAAGCTTGGCCGCATGG

09978298.101501

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSDRGSRMLLLLLLLGSGGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGGALWNRVPCFLRDWELQVHFQKIHGQGKKK
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDYTPNEEKQQERVFPYISAMVNNGLSLY
DHERDGRPTLGGCTAIVRNLYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

00070248.101501

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTGCTTAACCTCAGTGGGACTCCAAGATTCCAAGAAGAAATCAGTGTCTTTCATTCAAGRAAT
 TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAATCTGTCTTCTAGAAGAAATTTAAATTAATGCTGCACTCT
 GACATGTTCCCGATTGAGGTGAAACATGAAGAAGAAATAGAATCTTAATATGGCTTTTCGCAACCCGGCTCT
 TGCTGCTCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCCTGCACTTCTCCACCTGATCCCGGTG
 CGACTCTTAAGAATGGAATGAGTAGGACAGAGTCGAAGAGAAATCATGCCCGACCCCTGTGACGGAGCCCGCTGTGA
 CAGACCCCGTTTATGAGCTCTTTTGTACTGCACATCCCGAGTGGCCGAGCGCAGCATGGAAGGTCATGCCCT
 CGCATCATTTTAAGCTGGTCTCAGTGATGTGTTTCATTCGCCAGCGAGACAGGTACCCCATCTGATGTGTCATTCCCA
 AACAAGAGCGACAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
 TTAGTCACATGTCAAAAGGATCGGAGCCTCTTTGCAAGGCCCTTGAACTCCTTGGCTCTTTACCCAAATCACC
 CATTTGTGTGAGATGGGAGAGCTCACACAGCAGGAGTTGTGCAGCATTTGCAGAACGGTCACTGCTCGAGGATA
 TCTATCTAAGAGAAACACAACTCTCTGCCAATGATTGGCTGCGAGACAGCTCTATTAGAGACCCTGGGAAAA
 GCCGGACCTCAAAAGTGGGCTGGCCTTGTCTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTATTTTCA
 GGCACAGCCAAAGTGGCTGTCTGTCTGTGGAAGCTGCTATTGGCCGGTAAGAAACAGATATCTGGAAGAGGAGC
 AGCGTCGTGAGTACCTCCTAAGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAAGATCGTGG
 ATGTCCTCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
 TTCCCTGTACCAGAAATGGCTGTGTGACATGGAGCACTTCAAGSTAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAGAATTTGACTTCGGGTATTCTCTCCGGGTGCCACCCCATCTGACCCAAACCATCG
 GCCGGATCGACGCTGCCACCGAGGGCAGGAAAGAGAGCTCTTTGCCCTTACTCTGTCTCATGATGTCACTCTGT
 CACCAAGTTCTCAGTGGCTTGGGCTTTTCAAGGCCAGGTTCCCAAGGTTTGACAGCCAGTTGATCTTTGAGCTTT
 GGCAGACAGAGAAAGCCCAAGTGAACATTCGTCGGATCTTTACAATGGCGTCGATGTCACATTCACACCT
 CTTTCTGCGCAAGACCCACAGGGTCTCTCCAGGCCATGTGCCCGCTTGAAACTTTGGTCCGCTTTGTGAAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGTACAAATATTATGATGCATGTACAGGGAAGGATTCTAAAGG
 TATGCAATACAGCAATAGAAATCCATGCCAATACAGAGCATAGGGAAGGTCACATCTAGTTTGTCTGTTAC
 TAAGGCTAGAAGATTGCTTTTAAAGCTTAATATTGTTGTGGGAACCAAGCATGTTGGGGTGAACAT
 AAGCACATTCGCTCAATGTGGTACGTGAATTCGTTGGTACAAATGGCCAGTTACAGAGGAATAGAAGGTACTT
 TATCATGCTCAGACTTCGCTAGAAATGCCAGAAATAATAGTTCAAGACCTGAGGTTGCCAATGTTGTCAC
 TCTTCTGGCCTGGCCCATGTTACTATGTGATGGAACAGCACACCTCAACAAAATTTTAACTCTAGACATT
 TTTACCTTGTCTTGTGAAGATTCTTGAAGTGATTATCTAAAAATAGGTTGGCAACTTTTCTGTGAAGG
 GCCAGATTGTAATATTTCAGACTGTGTGACCAAAAGGCCACATCAGTCTCTGTCTAATACTACTCAACTCTGT
 TTTCTGAGCAGGAAAGCCACACAGACAGTACATAAAGGAATATGTGTAGCTGGTTCACAGCCAGACAAACA
 GATGTTGACCAAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATCTACAAATTC
 ACTTCAGCACTTTGAGAAGAGTTGAATACCAAGAAATATTCAATGGTCTCTCAGTAACCTCTGCTAGAAACA
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAATAAACAATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAATACTTGTATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTGT
 CTGCTGTAGTCTATTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAAATTT
 TTCTAAGACCAAGTTTATGATGACTCTTATCTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATTGAGCACTTTCTCCAATAAACTAATATGGCTATTCCCTTTGACAAGCTGTAGA
 ACTGGAATCATTTTTAAACCAATTTTCACTAGTTTCAATGGTAATTTCTGATTGATTTTTAAATGCGTTTTTGA
 AGAATTTTGTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTTAATTAACATCTG
 TGATTTCTGAACTAATGGTGTAAATCAGAGAAATGGAAGTGAAGTGAGATTTCTGTGTTGTCATCGGCATTCC
 AACTTTTTCTTTGTTTTGTCAGTGTGCAATTTGAATGTCTGTTTTCTATAAATAAATTTTTAAGATAAA

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALAALLAFVSLQLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSL LGAHPI LNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLENLVRVFKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

00078200-11501

[illegible][illegible]

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGLTLWETGCTQIRYSVPPELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRGTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDIIMEDKVKIYGVVEVEVR
DINDNAPYFRESELEIKISENAATEMRFFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYISLVTDIVLDREQVPSYINITVTATDRGTPPLST
ETHISLVNADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPCENNAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGFLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLES
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHVSLTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLSGDSVFSKDSHGL
IEVSLYQIFFLFFNCVSVQAGVQRYDHSSLRPQTPRLKQLSHLCRCNRD YRCKPPTVCL
IYLSIYLSIYLSIYLLSCTDGS LTPVIPVLWEAEAGGSPEVGS L RFA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCAAGTGCACAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGTGGCAACTGGGTCTT
ACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTACCAGTCCCCGAGAGAATTTCTTGACACTCTCAACT
GTGCAGAAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQLLCGGVL
VGGNWVLTAAHCKKPKYT VRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCG
CGCGCGCCCCACGCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG
GCCCGCGCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCGCGCCCCCGCCCCCGCCCCG
CCCCGGCCGGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACTGATCCCATAAAAA
ATTTCATCTCCCGGGCGCCCGCGCTGCGAGCGCCCCGCGAGTCCGCGCCCGCGCGCCCTCG
CCCTGTGCGCCTGCGCGCCCTGCGCACCCCGCGCCCGAGCCAGCCAGACCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGCGCGGCCCGGGCGCGGCCGTAGCGCGCGCGCCTGGA
TGCGGACCCCGCGCGGGGAGACGGGCGCCCGCCCCGAAACGACTTTCAGTCCCGCAGCGCG
CCCCCCCAACCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGTGTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGTGGCCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTGCCACATTCCACGGCCTGGGCCCGCTACACACGCTGCACCTGGACCGC
TGCGGCCCTGCAGGAGCTGGGCCCGGGGCTGTTCGCGGCCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGGCAACCTCA
CACACCTCTTCTGCAGCGCAACCGCATCTCCAGGCTGCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGCTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCGATGCCTT
CCGTGACCTTGGCCGCTCATGACACTATCTGTTTGGCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGACGCCCCACTCTGGGCCTGGCTGCAGAAAGTTCCGCGGCTCCTCCTCCGA
GGTCCCTGCAGCCTCCCGCAACGCGCTGGCTGGCCGTGACCTCAAACGCGCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGTGACAAGGCGCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGCGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCCCTTGGGACTCTG
CCTGGCTGTGTGAGCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCGAGGTT
CCCCACTCGGGCCCTCGCCGGAGGCCAGGCTGTTTACGCAAGAACCGCACCCCGAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGTCTCTCTCCACGCGGCCAAGCCAGCCGGGCGGCCGACCGTGGGGCAGGCCAGGCCAG
GTCTCCTCGATGGACGCGCTGCCGCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGACGCTTTGTTTCCAGAACGCGCCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGAGTGAATAAAGAGCTCTTTCTTAAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQQLQAVFVGIPAAQSRI
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCGELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNVRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLLNDNPFWVCDRCARPLWAWLQKFRGSSSEVPCLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAKASVLEPCRPASAGNALKGRVPPGDSFPGN
GSGFRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

2025

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
 TCACTTGGCATATTTCTGAGGATCTGTGAGTAATAACACAGCCTCAGATATGGGGACCTTAC
 AGTCCACAGAAACCGCTCTCCAGGAAGCTGAATCTCAGCAAGAAACAATGGAGGCCAGCGGGA
 AGCTCATTTTGACAGCAAAAGCCAGTCCCTTTTTCCTTCTCTCTTTTGGGCTTATCTCTGGCG
 GGCGCGCGCGGAACCTAGAAAGCTATTCTGTGGTGGAGGAAACTGAGGCGAGCTCTTTGTAC
 CAATTTAGCAAAAGGACTCTGGGTCTGGAGCAGAGGAAATTTCTCAGCGCGGGGGTTTAGGGTTG
 TTTCCAGAGGGAAACAACATACATTTGACAGCTCAATCAGGAGACCGCGGATTTTGTGCTAAAT
 GAGAAATGGACCGTGAAGATCTGTGGCGTACACAGAGCCCTGTGTGCTACGTTTCTCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGAC
 ACTCTCCAGTATTTCTGGACACCAAGAACTGTGGTGAAGATATCAGAGAGCAGTCTCTCTGG
 ACTAGCTTTCTCTGAAGAAATGGCAAGACTAGATGTAGGCCAAGAAACATATTTAGAGACTA
 TATAATCAGCCCCAATCTCTTATTTCTCGGTCCTTACCGCCAAACGAGTATGTCAGGAATA
 ACCCAGAGCTGTGTCTGGACAAAGCGCTGGACCGGAGGAAGAGCTCAGGTTTAAACA
 CTCACAGCATGGATGGTGGCTCTCCGCCAGATCTGBCACTGTCTCAGGTTACATCGAAGT
 CTTGGATGTTCACGAGATAATGGCCCTGAAATTTTGTAGCAGCTCTTCTATAGAGTGCAGATCTCTG
 AGGACAGTCCGGTAGGCTCTCTGGTTGTGAAGCTCTCTGCCACCTGATGATAGACAGGAGTCA
 AACGGAGAGATTTCTTATTTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
 CAATCCCTTTGACAGGAGAAATGAACTATGAAATAACCACTCGATTTCTGAAAAACTTCAGTCT
 ATGAAGTCAATATTAGGCAGAGAGATGCTGGAACCTTTTCTGAAAATGACCGTTCTGATT
 CAAGTGATAGATGTAACAGCATGCCCCACAGAAGTTACCATGTCTGCTATTACACGCCAAAT
 ACCTGAGAACCGCGCTGAAACTGTGGTTGCACTTTTCACTGTTTTCAGATCTTGATTCCAGG
 AAAATGGGAAAAATTAGTTGTCTCAATTTCAGGAGGATCTACCCTTCTCTCTGAAATCCGCGGAA
 AACTTTTACACCTCTAACCAGGAGAGACACTAGACAGGAGAAAGCAGAGCGGAATACACAT
 CACTATCAGTCTACTGATTTTGGGACCCCTATGCTGATAACACAGCTCAATATGACCTGTG
 TGATGCCCGATGTCAATGACAACGCTCCCGCTTACCCAAACCTCTACACCTGTTCTGCTC
 CGCGAGACAACAGCCCGCCCTGCATCTCCGACGCTCAGCGCTACAGCAGACAGAGACTCAGG
 CACCAACGCCAGGCTCACTACTCGTCTGTGCGGCCAGGACCGGCACTGCCCCACAT
 CCTTGCTCTCCATCAACCGGGAACAAGCGCACTGTTTCCGCCCTCAGCTCTCTGGAATCAGG
 GCGCTGTGAGGGTTCTCAGTTCTCGCGTGGGCGCTCAGACACGGCTCCCGGCGCTGAGAC
 CGAGGCGCTGGTGTGCGGTGGTGGTCTGGACGCCAACGACAACCTCGCCCTCTGCTGTGAC
 CGCTGTGACAAGCCGCTCCGCGCCTGCAACCGAGCTGGTGCCCGGGCGGGCCGCGGTAC
 CTGTGTGACAAAGTGGTGGCGGTGGACGGCACTCGGGCCAGACAAGCTGCGTGTGTGAC
 GCTGCTCAAGGCCACGAGCTCGGTCTGTTCGGCGTGTGGGCGCAACATGGCAGAGGTGCBCA
 CCGCCAGGCTCTGAGCGAGCGCGACGCGGCCAACGACAGCTGTGTGTGCTGTTCAAGAC
 AATGCGAGCGCTCCGCGCTCGGCAACCGCCAGCTGCACGTGCTCTCTGGTGGACGGCTTCTC
 CCAGCCCTACCTGCTCTCTCCGAGGCGCGGCCGACCGAGCCAGGCCAGCCGCTCTCAGCT
 TCTACTGTGTGGTGGCGTTGGCCTCGGTGTCTTCTGCTCTTCTCTTTTCGCTGCTCTGTGTT
 GTGCGGCTGCGGCTGTGTAGGAGSAGCAGGCGCGCTCTGCTGGGTGCGCTGTGTGCTCCGA
 GGGCCCCCTCTCAGGGCACTCTTGTGGACATGAGCGGCACGAGCCCTATCCGAGAGCTACC
 AGTATGAGGTGTGTCTGCGACGAGGCTCAGGAGCAATGAGTTCAAGTTCTCTGAAGCGGAT
 ATCCCCAATCTCCCTCCCCAGTGCCTGGGAAAGAAATACAGGAATAATCTACCTTCCCCAA
 TAACTTTGGGTTCAATATTCAGTGAACATAGTCACTTTACATTCATAGTATTTTATTT
 TGTGGCAATTTCCATGCCAATGTTTATTTCGCCCAATTTGTGTGTATGTAATATTGTACGGAT
 TTACTCTTGATTTTCTCATGTTCTTCTCCCTTGTGTTTAAAGTGAACATTTACCTCTTATT
 CCTGGTCTCTT

FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCGCTAGCCGTGC
GCCGATTGCCTCTCGGCTGGGCAATGGTCCCGGCTGCCGCTCGACGCCGCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
AGGTGTCAGAGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAAGTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCCATAATTTTATTATTTCAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACCAAGCCGACCAAATAGGCCCTCTTCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGATTTCCTTATTTCTTTTAAATTAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAGAGGAATTCATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTGACTTGAAACTTCAGGCAGATTAAGAAGATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCTGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNOTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCTCTC
TTTGCCAGCCCGACTTCTCTTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCCCCCGCTGCGCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTACCAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTTA
GTCCCCGGCATCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC
GGGATCTCAGTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGACGTTTGATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAACATAA
AAATCATGAATATTTTAA

00975293.101501

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCGSGARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSLCVQVKDR
CAPVMSAFGFFWPDMLECDRFPQDNLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSEKDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGLVITSVKRWQKQREFKRIKRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGCGGGGCCGACGGAGGCCGAGACG3GGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGTGGGTGTTCTGTCTCGCGATC
AGCCTGCTCAACTGCTCCAAACGCCACGCTGTGGCTCAGCTTTTGACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGGGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACCTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTGGGACCCAAAACCCATTTGCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCACAGAGCACCAGCGA
GCCACGCCAACATGCTCGCCACCATGTCGAACCCCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTGG
CCCTCTGCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCATATGTCACTCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCATCCAGTGGGTTTTTC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTCTCTGTG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTITGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGGA
GTGTTCTTCCCGTGGGGGAGGGGCTGCCACAGGCATGATCTTTGTGCTGGGCGAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCACGCTCGGAGCCGTCTCTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGACACGGCGACTCCGGA
GTGCACGCGCAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGTTCCACCTGCGGGCGGGGCGAAAGGGCTCCTTGGCGGT
CCGGAGCGAATTACAAGCGCGCACCTGAAAA

00076206 101501

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLV
KKGEDIPMLGVYITIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQ LQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAAATGMIFVLGQAEGILIMLAMTALTVRREPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEVPSTVIGKLSQELGRBERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRDLREQLCRQWDPLCVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPDLRALDPDTGPNTLHITYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDNSNDNSPAFAESS
LALAIQEDAAPGTLTIKLATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDNDNIPSIIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLTLLAQD
QGLQPLSAKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQORSLNYEEMAGFEFQVIAEDSGQPMLASSVSVVWVSLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLITTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHQKADIHLVPLRGQAGEPCEVGQSHKQVDKEAMMEA
GWDPCLQAPFHLTPTLYRTLNRNQNGAPAESREVLQDTVNLLFNHPRQRNASRENLNLEPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGGFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGQTDPEQEELDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFTQTFGKAEBEPLSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAAEALRRLSVCGRTLSLDLATSAAAGMKVQGDGPGGKTGTGEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCGTGTGCCCCAGCGTGCCTGTGGCCCTCGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCTTTACACTTCGCCATGAGTTCTCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAATTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGAATTTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCATAGAACAGCTCATCAGCCGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTTCTGGAITTTGGTGTCTCAACTGCCCATACACTTACATGTCTTACTTCTC
CAGGAATGTGACTGACACGGATACTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAAACATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTAATTTTCTTGTTACTTTTCTCTATTTACTGTGTTTGGAAAATTT
CATGGCTACCATCAATAITGTTTTTGATCGAGTTGGGAAACGGATCCTGTGACAAGAGGCA
TTGAGATCACTGTGAATATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATCTCTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCAATTGTCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAACTCACTGAAGTCCTTGGAAGTGCAGTTCAACTTCTATCACCCTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCTTCCCCGTCAAGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFPMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPFILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFGWMIKSVTTSASGSENLTLIQ
QEVDALELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

00070000 1015001

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNAGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCAACCATGTTTGAGCTCATCATCTTTGAAATCTINGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

09070208-101501

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTNNGNATACCTTCCAGAAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTGAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCCTC

00076298-101501

FIGURE 176

CTCGCCAGGGATCGTCCATGCGCGGGGCTCGGAGCCGCGACCCTTGGGGGGCTCCGGGATTGCTACCTTT
 TGCGTCCCTGCTGCTGGAATGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTCTTGCGCAA
 GGAGGGCGAGCCAGGACGCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTGTCAGCCCCAGCCCAAGCTG
 GCTGTGTTGGTGGTGTCCCGAGGCCCTGGCTCTTCTTGGGAGCAGGCGAATGCACTGTGAGGCTCTTGTGCTG
 CCGGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACAGGAGAGCTGATATGCAAAAGGAAAGCAA
 GGGAACCAAGTGGTGGGAGTCACTGTTCCGAGCCAGGGCTGGGGGCAAGATTGTTATCTGTGTCACACGATA
 TGAGGCAAGGACGAGTGGACAGATCTCTGGAGACCGGGGATAATGATTGGTCTGCTGCTTTGTTGCTCAGCCAGGA
 CTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTCTCTGAGGGACGCCCCAGGCACTGATGAACAAAT
 TGGGTTCTGCGCAGCAGGCGACAGCTGCGCGCTTCTCCCTGATAGCCACTACTCTCTCTTGGGGCCCCAGGAAC
 CTATAATTGGAAGGCGACGCGCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGACACTGGCACCTGTGACGACGG
 TCCCTACGAGGCGGGGGAGAGAGGAGCAGGACCCCCGCTCATCCGGTCTCTGCGCAACAGCTACTTTGGCTT
 CTCTATTGACTCGGGGAAGGCTCTGGTGGTGCAGAGAGGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCACACCA
 CAAGGGTCTCTGGTCTACTCTGCGCAAGGACAGCGCCAGTCTGCTGGTGGTGGGCTTATGCTGTCTCTGGGAGCG
 CTTGACCTCCGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGCTGGCCAGACCTGATAGTGGG
 TGCCCCCTACTTCTTTGAGCGCCAGGAAGAGCTGGGGGGTGTCTGTATGTGACTTGAACAGGGGGGTGCTG
 GGCTGGAGTCTCCCTCTCCGGCTCTCGGGCTCCCTGACTCCATGTTTGGGATCAGCTGGCTCTCTCTGGGGAG
 CCTCAACCAAGATGGCTTTCCAGATATTGAGTGGGTGCCCTTTGATGGTATGGGAAGCTCTTCACTACCA
 TGGGACAGCTCTGGGGTTGTGCGCAAACTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCCG
 CTACTCCCTGTCCAGGCACTTGGATATGGATGGGAACCAATACCTGACCTGGTGGCTCCCTGGCTGACAC
 CGAGTGTCTCTCAGGGCCAGACCCATCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATGACCT
 GGAGAGCCCAACTGTGTGTCGGGCCACTCGGTCTGTGTGGACTTAAGGCTCTGTTTCAGTCACTTGCAGTCCC
 CAGCGTGTATGGCTTACTGTGGCCCTGAGCTATGTGTAGATGCGGACACAGACCGGAGGCTCTCGGGGCGAGT
 TCCCGCTGATAGCTTCTGAGCGGTAACTTGAAGAACCAAGCACAGGCTCTGGGCAACCGTGTGGCTGAAGCA
 CCGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGAAGAGCTCTGGGCCATTGT
 AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCTGGCCAGGGGCTGCCCTCAGTGGC
 CCCCATCTCAATGCCACAGCCAGCCAGCACCCAGCGGGCAGAGATCCACTTCTGAAGCAGGCTGTGGTGAAGA
 CAAGATGTGCCAGAGCAATCTGCAGCTGGTCCAGCGCCGCTTCTGTACCCGGGTGAGCGACAGGAATTCGAACC
 TCTGCCATGGATGTGGATGGAAACAGCCCTGTTTGCACGTGAGTGGGCGACGCTCATTTGGCCTGGAGCTGAT
 GGTCAACCAACTGCTCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCTGGT
 CATGCTCTCTGACTCACTGCACTACTCAGGGGTCCGGGCTGGACCTCGCGGAGAACCACTCTGCTCTGCTCAA
 TGGAATGCTCTCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACTCTCAT
 CCTTAGCACCTCGGGATCAGCATGTAGACCAACGGAATGGAGGTAGAGTGTCTGTGGCCAGATGAGTGAGCA
 GGAGTGCATCCAGTCTCTGCAACAGCCGCTGTCTTCTATTGAGCTGCCATGTTCATTGACGAATGGCATTCC
 CCAGCCACTCTTCTCTCTGTGGTGGTGGGGGCGAGAGAGCCATGAGTCTGACGGGGATGTGGGCGAGAGGT
 CAGTATGAGTCAAGGTTTCCAAAGGCGAGTCCCTCAGAACCTCTGGGCTCTGCTTCTTCAACATCATGTG
 GCCTCATGAGATGCCAATGGGAAGTGGTGTCTGTACCAATGCAAGTGTGAGCTGGAGGGCGGGCGGGGCTGG
 GCAAGAAAGGCTTTGCTCTCCAGGCCCAACATCTCCACTGATGTGAATGTGAACAGGATAGAGAGCGCGCGGA
 GCTGGAGCCACTGAGCAGCAGGAGCTGGTGGGCGGAGGAGCCAGCATGTCTGGTGGCAGTGTCTCTGTC
 TGAGAGGAAGAAAAACATCACCTGGAAGTGCGCCCGGGGCGAGGCCAACTGTGTGGTGTTCAGCTGCCACTCTA
 CAGCTTTGACCGCGCGGCTGTGCTGCACTGTCTGGGGCGGTCTCTGGAAACAGCACTTTCTGGAGGAGTACTCAGC
 TGTGAAGTCCCTGGAAGTGTGTTGTCGGGCCAACATCACAGTGAAGTCTCTCAATAAGAACTTGATGTCTCGAGA
 TGCTTCCACAGTCTCCAGTGGTGTATCTTGAAGCCAGGCTGTGGTGGCAGAGGAGTCCGCTGTGGTGGT
 CATCTCTCTGTGCTGATCCGCTGGGCTGTGTGTGCTAGCACTGCTGTGCTGCTCTCTTGAAGATGGGATTTCT
 CAACCGGCGAAGCACCCCGGGCCAGCGTCCCCAGTACGTGCGTGAAGATTCTCTGGGAAGAGCAGCAGCA
 GTTCAAGGAGGAGAAGACGGGCAACCTCTGAGGAACAACTGGGGCAGCCCGCGCGAGGGCGCCGATGACAA
 CCCCATTGCTGCTGTGACCGGCACTCCGAGCTGGGCCGATGGGCTCAGCCCGGAGGACCGCCCTAGTCTCC
 CATGTCCAGCCCTGGCTGTGGCTGCGCTCATCTCTTCCACAGAGATGGCTCTTGGGATGAAGAGGTGAGT
 GGGCTGTGGTGTGCTCATCAAGATTGGCAGGATCGGCTTCTCTCAGGGGACAGACCTTCTCCACCAAGAAC
 TCTCTCCACCCACTTCTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGAACAGGGCCATGGGCTAGGG
 TGAGAAAGGCGAGGGGTGCTCTGATGCAAGGTGGGGAGAGGGATCTAATCCCTTCTCTCTCCCTACCTGT
 GTAAACAGGACCCAGGACCTGCTCCCGGAAGTGTCTTAACCTAGAGGCTCGGGAGGAGGTGTGTCACTGA
 CTACGGCTGCTCTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGATCAGTCTAGTGGTTTCTGGT
 TCTGCTATTATTAAAAAATATTGAGAACAAAAAATAAAAAAAAAA

00076206-101501

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGFLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPQGGKIVTCAHRYEARQQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKCEG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTS GFYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGI
SPRLRCGSPDSMFGISLAVLGDNLNQGFPDIAVGAPFDGDKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSGYSLSGSLDMMDGNQYPDLLVGLSADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCDLRLVCFYSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPOSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQQAQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGPNPMKRGAVTFYILSTSGISIEETLEVELELLATISEQELHPVSARARVF
IELPLSLAGMAIPQQLFFSGGVVRGERAMQSERDVGSKVKEYEVTVSNQGLSLRTLGSFAFLNIM
WPHEIANGKWLLYPMQVELEGGQGPQGKGLCSPRPNILHLDVDSDRRRRRELEPPEQPEPGE
RQEPMSMSWPPVSSAEKKKNTLDCARGTANCVVFSCLYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPMVAVVAEGVPWWVILLAVLAGLL
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGITILRNWWSPPREGP
DAHPILAADGHPGLGPDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCCGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCAGTGGTCTATCCAGCCCTGTTTGTGGTTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAAACAGATCTCAGTCAAATGTGAAGGCAATTGC
CCATGTCCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT
GCTATTGGACCAAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCCTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTGTCAGGAGTGTGGACAGTGTGCTGTGTGTTGACAGATATGGAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTGAGTTGATGACAGTTGAAATCAATAAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGATCATTTTGCTTTGAGTTTTTATATTCTTACACAAAAAGAAAATACATATGCAGTCTA
GTGACAGAAAAATAAAGTTTGAAGTGCTACTATAATAAATTTTTTACAGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATTTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCAATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAAATAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCQPVVYPSVPCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRPERSRFDTSILPI
CKDSLGMWFMNRLDTNYDLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPQCQTELSNIQKRQGVKLLGQYIPLCDEDDGYKPTQCHGSGVQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
 CTCITTCAGCCCGGATGCCCCAGCAGGGAATGGGGGACAAGATCTGGCTGCCCTCCCGGTGCTCCTCTGGCCG
 GCTCTGCCCTCCGGTGCTGCTGCTGGGGCGGCGGCTTCAACCTTCCCTCGATAGGAGCTTACCTTTTACCTTT
 CCGCGCGGCGGAGAGGATGCTTCTACAGCCCATGCCCTGAAGGCTTCGCTGGAGATCAGTACCAAGTTTAT
 GATGAGACAGATTTAGATATTTTTCATCTTGGCTCTCAGAAAGCAAAACCTTAGTTTGTGAACAAGAAAA
 TCGATGGAGTTCATCATTTAGAGATCGAAGTTGGTGATTACATGTTTCTGTGCAACATACATTCAGCACCAT
 TCTGGAAGAGTGAATTTTCTTGAATTAATCCTGGATAATATGGGAGAACAGGCAACAGAACAGAGATTTGGAAG
 AAAATATATTACTGGCAGAGATATTTGGATATGAACCTGGAAGACATCTGGAATTCNTCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCAACATACAAATTCGCTTAGAGCATTTGAAGCTCGTGATCGAAACATCAAGAAAGC
 AACCTTGATAGAGTCAATTTCTGGCTTAGTGTAAATTTAGTGGTCAATGGTGGTGGTTCAGGCCATTCAGTTTAT
 ATGCTGAAGAGTCTGTGTTGAAGATAAGAGGAAAGTAGAAGCTTAAAGCTCCAAACTAGAGTACGTAAACATTGAAA
 AATGAGGCATATAAAATGCAATAAAGCTGTTACAGTCAAGACCATTAATGGTCTCTCCAAAATATTTTGAGATATA
 AAAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
 TTGTACTTAAGTGTGTAACAGGAATATTTTCAGAAATATAGGTTTAACTGAAATGAAGCCATATTAATACTGATC
 TTTCTTAACCTTTGAAAAATTTTGAACATGCTTAGGTGATTTAAATAAATAGATTTGGGCCATAATTCGAACACC
 AGTCTGTTTTTAAACAGTTCTATATACCCAGAAGCTTTTGTGAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
 TCAGTTTCTTAAGTTATAAATCACCTGAGAAATACCTAATGATGGATGAATAAATCTTTAGAGTACAAAAGCCCAA
 CTTTTTCTCTATTTACAAATGACATCTCTCTATAATGTAATAGAAATAGCTTTGAAATACAAATTAGGTTTATTC
 AGATTTTATAACCAATACATTTTCAGTGTAAACATTTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
 CCAAAGCTGACATTTTCAGGATTTCTTAAACCAAAAGTTACACTTACTTAAATTAGGACATGTTTTCTCTTTG
 AAATGAAGAATATAGTTTAAAGCTCTCTCTCCATAGGACACATTTTCTTAAACCTTAACTAAAGTGTAGGA
 TTTTAAATTAATGTGAGGTAAATAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAAATTTTAAACATGATTGCTGACTGGATAATTCATATTACCAGCAGTTATGAAGGAAATA
 TTGCTAAATGATCTGGGCTACCATAAATAAATATCTCTTTTCTGAGCTCTAAGAATTATCAGAAAAAGGAA
 AGAATTTAGAAAACTTGAGAAAACTTAATCCAAATAAAATTCATTAAGTAGAACATATAAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCTCTCATACATAAAATCAAGGAGATGATTAAATTCAGTTAGCTGGAAG
 AAACCTTTGGCTGTAGGTTTATTTTCTCAAGAAATTCGGTTTGAATATTTTTTGAAGCAGGATACATTTTATA
 AAATGAAGCCCTTCTGTAAAGTTTTCAGTGGGTGATCAATATTTTAAATTTTATATAACCAACTTTTAT
 TAAATATGCTTATCTGACCACTTTTATTTATGATGTTGAAGTAAAGATTAGAAACATGACTCCCAAGTTTATAA
 CACTAAATGTGAATAACCATATATACAAAGAAATTTCTGCCATCTAGCTTTTGAAGTCTATGGGGCTTTAC
 TCAAGTACTAGTAAATTTTATCTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTTATAAGCTTTGTTAT
 GACTCATTTGTGAGTTAGAAACAAACTTAAATTTGGGCTATAGAACCCCTCAACAGGTTAGTAATCTGGAAT
 CTGTATGAGCAATAATGATAACAGAGAGTGATTTCAATTACCTCATAGTAGTATAAAAGACATCAATTTCCC
 TCTTAGGCCCCCTGGAAGAGAGCAGCTTAGATTTCCCTACTGGCAGGTTTATAAATGAGGTAAATGGCGGTAT
 ATGATCAATTACCTTAATTTGGCCAGAAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACCTTCGCAACA
 AGGTCAATAAGATCTCTGCCTATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGACACAAAGTAAAAAGACAGATATTTAGAGG
 CATACCAAAAAAGCAAACTTTGTAACAGAGTAAAACTTTAATATTTCTAAGACATACCTGTTTATCTGCTT
 CATATGCTTTTTTAAATTTTCACTTTTCCATTTCTAAATTAAGATTATGCTCAAAATTTGGATGCAATTTGATCACTT
 AACAGCTCATTTTGTCTTTTTCATATACAAATTTTAAATAATCTACAAATTTTAACTAAGGCCCAACCGATTTC
 CATTAATGTGAGGTTTACCGTGTTCACCTCAACACTAAGGCCCTAGAGTTTGTCTGATATGCAATTTGGATGATTAAT
 GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGTTGTTGTAATTTTATGGTAAATTTAATCCTTTCTA
 CACATAATGGTGTCTTAAATTTGACAAAAATAGGACATCTCAATTTGATGATGATCTGCTCCTCAATGAAGATCTTTAT
 GTGAAATTTTAAAGACATGATGTCGCATGTAAGGATTTTTCATCTGAAGTACATAAAGTCAACATCAGTGTGTTG
 CTCAAACTGCTTTTATACCTTATAAACAGCATCTTAAATAGCAACGATTTTGTAGTACTGATATGATATAATAA
 AAATATCATAGAGAAAA

097328.101501

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
```

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLSDSFTFTLPAQKQCEKYQPMPLKASLEIY
QVLGDAGLDIDFHASPEGKTLVFEQRKSDGVHTVETEVGYMFCFNTFTSTISEKVIFEL
ILDNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN
IOESNFDRVNFWMSMVLNVVMVVSAIQVYMLKSLFEDKRKSR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FIGURE 182

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGT CAGGTTCAAGGTGAAGAAACCCAGAAGGAAC TGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCAACAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTC AAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGT CATGATCCTCC
TTCTTTTCCCTTTTCTTCACCTTCATTT CAGGCCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

007500-101601

Figure 1 illustrates the steps of the proposed algorithm for finding a minimum spanning tree. The process starts with a graph with 10 nodes and 15 edges. The algorithm proceeds by selecting edges in increasing order of weight, rejecting those that either create a cycle or result in a vertex with a degree greater than 2. The steps are as follows: (a) Initial graph; (b) Select edge (1,2) with weight 1; (c) Select edge (2,3) with weight 1; (d) Select edge (3,4) with weight 1; (e) Select edge (4,5) with weight 1; (f) Select edge (5,6) with weight 1; (g) Select edge (6,7) with weight 1; (h) Select edge (7,8) with weight 1; (i) Select edge (8,9) with weight 1; (j) Select edge (9,10) with weight 1; (k) Select edge (1,3) with weight 2; (l) Final minimum spanning tree with 9 edges and total weight 9.

<subunit 1 of 1, 175 aa, 1 stop

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSLSGABGSFVSSLVRSISNSYSYIWIGLHDPQTQGSPEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGCCCGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCCAACCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

0976293.101501

FIGURE 185

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405
```

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FOGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTFCGCGATGG
TAGCGCGGGTCTCTGGCGGCCACCCTCTGTCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCCGCGCGGGGAATCCTGTACCCGGGCGGGGAATAAGTACCAAGACCATTTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCA CGCTATGTGTCTGCCCGGGAATTA CTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTGTGTCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGA CTAGAAATATTCAGCGTTGTACTGTGGAGAAGGTCTGTCT
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTTCTTAGGCTTCACACTTGTCTAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTATATAATAGATGCTATGAAAAC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATCTCAGTGTGGCATTACCTGTAAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCAT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGKNKYQTIIDNYQFPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGVCTKRRRGSHGLEIFQRCYCGEGLScriQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

0970203-101501

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCGCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGNTT
CTGATCAAAATCATTTCCGAGGAGAAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

00972226-101501

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCGCGGTGTGGCTGCACCTCACCACCTCCCGTGCGCCGCGG
 CTGGGCGGTGGAGAGTGGCTGTGCTTCTCTCTGCACGCGGTGCTGGGCTCGGCGAGCGGGGTCCGCGGCCA
 GGGTGTGAGGATGGGAGGTAGCTACAGGAAGCGACCCGCGATGGCAAGGTATATTTTGTGGAATGAAAGGA
 AGTATGAGAAATGAGCTGAAGACCATTCACAGATTAAATTTTGGGGACAGATTTGTGATGCTCTGATTCACTT
 TGAAGTAATGTACAGAGAATCTCAAAATTTGCAATATTAATCACTGGAACCGACAGGTGAATCTTAATGTCTAC
 TTAATCAGAATCTGCATAAGAAAGAAATGGAGTCTGGTTAAATAAGAGTACTATATCAGAGACTTGAAGAA
 GATCATTCTCTGTTTTCTGATGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTCAGTTTACTTGG
 AGTGTCCAAAATGCAAGCAGTAGAGAAATAGACAGCTTTTCAAGAAATTTGGCATATGAAGTACTCAAAGTGAAGA
 AAACCCGGAATACCCAAATGCACATGGCGATTTTAAATAATAATAGAGCATATGAAGTACTCAAAGTGAAGA
 TCTACGGGAAAGATGACAAATATGGGAAAGGGGACTTGAGGATATCAAGGTGGCCAGTATGAAGGTCTGGAA
 CTATTATCGTTATGATTTGTATTTTATGATGATGATCTGAAATCATAACTTGGAAAGGAAGAAATTTGATGC
 TGCTGTTAAATCTGGGAACTGTGGTTTGTAAATTTTACTCCCAGGCTGTTCACACTGCCATGATTAGCTCC
 CACATGGAGAGACTTTTGCTAAAGAAATGGATGGGTACTTCGAATTTGGAGCTGTTAATCTGTGGTATGATAGAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTCATTTTTCGGTCTGGAAATGGCCCCAGTGAATA
 AGGAGAAATTTGTGCACTTCAACAGACAGCTCAGGCTTAGTGGCATGTGTTTCTCAACTATTGGTGTCTGAA
 AGAATAATATTTGGAAGTAATACATAATCTTCCAGATTTTGAACACTCTTTCGGCAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTATTTTTCATTTTGGAAAAATGAATAATCAATGATCTGAGCTGAAAAAATCT
 AAAAATCTACTTAAAAATGATCATATCAAGTTGGCAGGTTTGAATGTTCTCTGCAACAGACATCTGTAGTAA
 TCTGTATGTTTTCAGGCGCTCTTACGAGTATTAAGGAACAAGAAACCAAGAAATTCATCATGGAA
 GAAGATTTCTTATGATATACCTGCTTTGCGCAAGAAAGTGTGAATTTCTCATGTTTACCAAGCTTGGACCTCAAAA
 TTTTCTGCCAATGACAGAAACATGGCTTGTGATTTCTTTGCCCGCTGTGTCACCAATGGAGCTTTACT
 ACCAGAGTTAGCAAGAGCATCAATCTTCTTATGGTCAGCTTAAGTTTGGTACACTAGATGTGATCATGATGA
 GGGACTCTGTAGTCTATATAACATTCAGGCTTATCCAAACAAGTGGTATTCAACAGTCAACATTCATGATGA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
 ACCACCACTTCTCAAGCACTAGTTTACAAAGAAAGAACCAACAGCTTGAATGGTGTGATTTCTATTCTCCGTG
 GTGCTCATCTTCCCAAGTCTTAATGGCCAGAAATGGAAAGAAATGGCCGAGCAATTAATGGAATGATCAACGTTGG
 CAGTATAGATTTGCCAACAGTATCTTCTTTTGTGCCAGGAAACGTTCAAGATATCCCTGAGATAAGATTTT
 TCCCCCAAATCAAAATAAGCTTATCAGTATCAGATCTCAACACTCAGCTTTCAGTGAAAGTCTTACAGG
 CTGGGCTCAGGATTTTACTCTCAAGTATCCACAGATCTCAACACTCAGCTTTCAGTGAAAGTCTTACAGG
 GAAAAATCATTGGGTGATGATTTCTATGCTCTTGGTGTGGAACCTTGCAGAAATTTGCTCCAGAATTTGAGCT
 CTGCTGAGGATGATTAAAGGAAAGTGAAGCTGGAAGTGAAGCTTTCAGCTTTCAGCTCAGACATGCCAGAA
 AGCTGGGATCAGGCGCTACCACTGTTAAGTTTATTTCTACGAAAGAGCAAGAGAAATTTTCAAGAGGACCA
 GATAAATACAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATTTGGAACCTTCCGAATCAAGGCCA
 GAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAAAGGTTTAAAGAAATTTCTGACAGATGACATCAG
 AAGACACCTATTTGAATGTACATTTATGATGGGAATGAATGAACATTTATCTAGACTTCGATGTGACTGTCAG
 GAATTTATCTACAGCATCTGTGTGAAAGAGAGGCTCTGCAAACTTTTCTGTAAAGGGCCGGTTATATAATTTT
 GACTTTGCAAGCTATAATATATGTTTACACATGAGAACAAAGATAGAGTCATCATGTATTTCTTGTATTTGCT
 TTTAAACAACCTTTAAAAAATATTAAGCATCTTGTAGCTCAGAGCCATCAAAAGATAGGCTGAGATCAGTCATG
 GACCATAGATTTGCTGTCCCTTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCTTCAAGTTTTCGGCTGACCTGAGGAAAGTAACT
 TAGTTTTTGTGCTGTTCTCTTAAAAATGCTATCCCTAACCATATTTATTTCTGTTTTTAAAAACACCCAT
 GATGTGGCAGATGAACAAACCTGTTATGCTGTATTTATGAGGAGATTTCTCATGTTTTCTTCTTCTCTCA
 AAGTTTGAAGAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTAAATGTCGACACAGTAAGTACAC
 AAATTTGAGCAAGTAAATGTCGCAAAATCTGATGTTGCTGTATCATCAGGATAATCTGAGGTTTCTTCAAGTCTAT
 TAGCAATTAATCTGGGACTGTAGAGTATCTAAATATGTTATCAAGTATTAGAGTTCTATATTTTAAAGATATA
 TGTGTTCAATGATTTCTGAAATGCTTTTCTAGAAATTTTCCCATGATGATTTGTTTGGAGCATCTAATAT
 TTTACATTTGCTCTGCACTTTGTTTGGACGTGATCTTATTTACATTTGGGTTTTTCTTTCTATGTTTGG
 TTTTCTCATCTCTGCACTTATTTATTTCAAAATAGGAAAAATTTCTTCAAGTGTGTTTCAAGTGTCTAT
 AATGATCTGTAGTATTTCCAGTTACTAGTTTACTGTGAGAGGCTGCTTTTTCAGTAAATATGACATAAAT
 ACTGAAGTTTATTTAAGAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTTGA
 CTCAAAGAAATCAAAATTTGTGATACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGATGTTAAAAAT
 CCAATCAGTCAAAAGAGTCAATGAATTAAGGCTTGCACTTTTCAAAAAAAGAAAAA

00076293.1015001

[illegible]

<subunit 1 of 1, 747 aa, 1 stop

MGVWLNKDDYIRDLKIIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKPNPNNAHGDFLKNIRAYEVLKDEDLKKYDKYGEKLEDNQGGQYESWNYYRYDFGI
YDDDEPIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIIFRSGMAPVKYHGDRSKESSLVSFAMQHVRSVTVELWTGNFVNS
IQTAFAAGIGWLITFCSSKGGDCLTSQTRLRLSGMLFLNSLDAKETYLEVIHNLDPDFELLSAN
TLEDRLAHRWLLFFHFHGKNENSNDPELKKLKTLLKNDIHQVGRFDCSSAPDICSNLVYFQP
SLAVFKGGQGTKEYEIHGGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEGEGHS
AEQILEFIEDLMNPVSVSLTPTTFNELVPTQRKHNEVNMVDFYSPWCHPCQNLMPWEKPMART
LTGLINVGSIDCQQYSHSCFAQENVQRYPEIRFPFKPNKAYQSYNSGWNRLDAYSRLWGLG
FLPQVSTDLTPDQTFSEKVLQGNHNHWIDFYAPWGCQNFAPYFELLARMIKGKVKAGKVDC
QAYAQTCOKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGRNKDEL

Endoplasmic reticulum targeting sequence.

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCTCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTTGGA
GTCGTTGGTGAAAGTTTTTCATTCTCAGAGGAGAAAAATCTGTGGCTGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACCA
AAAATCCAAGCAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAAATGATTTTTGTTCATCGTATATCAATATCTTCTGAG
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCGATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTT
TCAGTCTGTATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTATAGGTCTGTTTTCTCCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAGGTTTTCTTTAAGATAT
TTTTATTTTCCATTTAAAGGTGGACAAAGCTACCTCCCTAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTTAAGACTGTTCAAGTAGCATTTCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCTTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCTCCCTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACTTTTTCTTTGTAAATTTATGCTTTTATATATCTTGGTCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAGGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA
CAATGGACCCAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETTDEVVRSLID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

3

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

00075233.101564

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCACGACAG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCCGGGG
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTA TCTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGCGGGCCGCCGCTGCCACAGCCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGACAGGATTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCACAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCGCGCGAGCAGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCAACAACGCGCAGCGCACCTGACCTTCAACAAGTTCTGGCGCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCGGTGCCATGTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTCGCCAACTTCATCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCTGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTCTCTTCGGCTACCCCCAAGCCCGAAAACCTCTCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTCTCGCGTGCCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACCTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTAAGATTAAATATATTTCAGGTATTTAATACGA

00376299.104501

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSVMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRDLTA
DSDVDEFLLDKFLSAGVKQSDLPKETEQQPAPGSMEESVRGYDWSRPDARRSPDQGRQQAER
RSVLRGFCANSSLAFFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDAAQLLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

TCCGGGCCAGAATTCCGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCTTGGTTTCTGAGACCATCCGCGGATTGGCCGCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGCCTGAGGAGACCTCTGCCACGGGATTCGCCACGT
GCTGGAGCTGAACCTACTGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCGAG
CCACTGGGGCCGATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCGATGTTCTGGCCCTCCGA
AGCCAACCTTCTGCACGGGCATTGAACTGCTGTCGAGCGGGGTCGACGATGGGCTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGGAGCAGCCCGATATCCCTTCTGATTTCTCTCATT
CTACTTGGGGCCCCCTTCTTAGGACTCTCCACCCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTTAAGCCACGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVITGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNVNAGHHPPQRPETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

09073293-103001

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCATCTTCTCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCCGCCG
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGGAATCACCTGGCCAGAAAGCCAGGCCAGCCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAACACTGACTTTTGAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNPFMTMQEDRSMVSVFVSQVPVRRRLCPPPPRTGPCRQRAVMTIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

0073208.101501

FIGURE 199

GCGCGCCGAGGCGTAGGCGGGGTGGCCCTTGCCTCTCCGCTTCCTTGAAAAACCCGGCGGG
 CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCCACTCCCGCCGAGAAGCCTCGCTCG
 GCGCCCAACATGCGGGGTGGCCCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT
 CGCGGCTGTGGCGGCGAGCGGAGGCCCGAGGAGCCGCGCTGCCCGCCGAGCAGAGCCGGG
 TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGAGGGCGAGTGGATGCTGAAATTT
 TAGCGCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA
 TGGTGAATAATCTCAGATCAGTGTGGGGAAGGTAGATGTCAATTCAGAACCAGGTTTGAGTG
 GCGCCTTCTTTGTCAACCACTCTCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGT
 TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
 AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
 TTTTATGATCTCTGGCAAGATATGGCATCTTCACAACATATTCACAGTGACTCTTGGAAAT
 CCTGCTTGGTGTCTTATGTGTTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
 TCTGGTCTTGGTGGTAAATATCAGAATGTTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
 GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
 GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAGACAGCCTTGTAGATGATGAAGAAGA
 GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
 CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
 ACCGGGAGGAGAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGC
 TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAAGTCAGCATGTGTACAAGGGAC
 TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCACTTCCCTTTGG
 CCTGCAAGTTTGTACCAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTAAAAGATGCT
 CTCTAGTCATTTGGCTCATGGCAGTAAGCCTCATGTATACCTAAGGAGAGTCTTCCAGGTGT
 GACAATCAGGATATAGAAAAACAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
 CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACAGAGGAGGCCATTCCCACTCTTAATC
 AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAGCCAAGCAGGAGCCTTGGCT
 CCTGAGCATCCCCAAGTGTAACGTAGAAGCCTTGATCCTTTTTCTGTGTAAAGATTTAT
 TTTTGTCAAATTGCAAGAAACATCAGGCACCAAGTGATGCAATGAAAACTTTTACAGCTAGAA
 ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
 TGCTATGTTTTATTTCTTACCTTAATTTTTCCAGCATTTCCACCATTGGGCATTCAAGCTCT
 CCACACTCTTCACTATTATCTCTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
 TGTGTTTGTTCATCTGACCTAAGGGGTTTAGATAATCAGTAACCATTAACCCCTGAAGCTGT
 GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
 TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAATATAGTTGTGTGATTTTTTTTT
 AAGTTTTCTAAGCAATATTTTCAAGCCAGAAGTCTCTAAGCTTGGCAGTACAAGGTAGT
 CTTGTGAAGAAAAAGTTGAATACTGTTTTGTTCATCTCAAGGGGTCCCTGGGTCTGAAC
 TACTTTAATAATACTAAAAAACCACTTCTGATTTTCTTCAGTGATGTGCTTTTGGTGAAA
 GAATTAATGAATCCAGTACCTGAAAGTGAAAGATTGATTTTTCATCTTCTGTAATC
 TTCAAAGAATTATATCTTTGTAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGAG
 GCTAATTTCTTT

09978293-101501

2019

<subunit 1 of 1, 349 aa, 1 stop

MAGGRCGPQLTALLAAWIAA VAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQPTDSEWEAFAKNGEILQISVGKVDVIEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISCEFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEK
DSDNEEENKDSLVDDEEKEKDLDEDEAEIEEEEDNLAAGVDEERSEANDQGGPEDGVTR
EVEPEEAEGEIS EOPCAPPTVEVDSLRKSHQADKGL

Signal peptide:

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTGTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCACTCAGGGGCAGAAAGAAAAGAGCTCC
CAAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAAATGGAATATCATCCTGATTTAGAAAAAT
TTGGATCAGAGATGGATATACATCAATTACACTTCGACTCTCAAAGCAATACAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTCTGCATCTCCTCTGGCGCTCATTTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTCGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCTCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTATAGTAAAAACAAGTGTCTTCCCAACTGATAATTCTATT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAAGCTTATTTTCAGATCAGAACCACAGCTACCCCAAGAAAACCCATCTCCAATTGTG
TATGGATTACAGTGTTCAGTCATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGCAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAAACAGAACAGAAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAAATG
TTTAGAGAGCTTGGCCAACTGTAATCTTAAACCAAGAAATGGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGCGACTACAGGTAGGCTAGTATTATTTTCTAGTTAGATAGTCTGACATCGT
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTATTTATTTATTTTATTTTGGAGATAGGGTCT
CACTTTGTTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAAATTTTGGTG
TTTTTTGTAGAGACTGGGTTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTGCCACGATTTTGACCTCAACTCTAGCAGTATATCAGTTATGAATCAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTAATTTTCATCAGTATGATCATAAATTATGATTATCATCTTAGTAAAAAGCAGGAATCCTA
CTTTTCTTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAACGG
CAGCATCTCGGCTCACCGCAACCTCCGCCCTTGGTTCAGCAATTTCTGCTGCCTCAGCT
CCCAAGTAGCTGGGATTACAGTCAGGCAGGCACCACACCCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCCTCGGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCATGCAACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAACCTGCTCTCATAGGAAGTTTCTGCTTTTTAAATACA
AAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTGTGATGTACTGTTTACAAATTTT
ACCATTTTTTTCAGTAATTAAGTAAAATGGTATTATTGGAATGAAACTATATTTTCTCATG
TCTGATATTGCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTTATTTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATATGCAGTTTAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGTTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

00078228-111601

FIGURE 203

GGAGGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGGACCTGCCAGACCTGGAGGGGTCTCGCTCTGTCA
CACAGCTCGGAGTCAGTGGTGTGATCTTGGCTCATGTAACTCCACCTCCCGGGTTCAAGATGATTTCTATGCC
TCAGCTCCCGAGTAGCTGGGATTAACAGTGGTGAATCTTCAAGAGTGACTCCGTGGGGGAAATAGACTCCCCAG
TCGCTGCTCAGACGACATGTTCCGCTGAGTGTGCTCTTCTGGTCCAGAGTGCCACAGCGCAGGGGCCACAGG
GAAGACTTTCCGCTTCTGACGCTCCGCGGAACACAGACACACAGGAGCAGCTCCACTACAAACCCACACACAGAGCTTG
CGCATCTCCATCGAGAACTCCGAAGAGGGCCCTCAGCATCTCATGCCCCCTTTCCCTCGACGACCCCTGCTTCCCGA
TCTTCTCCTGACCCCGAGGGGCCCTTACCACTTCTGCTCTTCTGGAACCGACATGCTGGGAGATTACATCTTCTC
TATGGCAAGCGTGACTTCTTGTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCAACGAGGAGGAGAGCGCTG
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCCTCTGGTGGAGCCTCAGAACATCAGCTGCCAGTGGC
GCCAGCTTCACTTCTCCTTCCACAGTCTCTCCCAACAGCGCGCTCACAATGCTCTGGTGGACATGTGCGAGCTG
AAAAGGGACTTCCAGCTGTCTGACGAGTCTCTGAAGCATCCCCAGAAGGCTCCAGGAGGCCCTCGGCTGCCCC
GCCAGCCAGCAGTTGAGAGGCTGGAGTGCAGAACTGACCTCTGTGAGATTTCATGGGGGACATGGTGTCTCTCGAG
GAGGACCCGATCAACGCCACGGTGTGGAAGCTCCAGCCCCACAGCCGGCTCCAGGACCTGCATCTCCATCCCGG
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCCTCGAACACTCTTCCAGAGGACGAAAGGC
CGGAGCGGGGAGGCTGAGAGAGACTCTCTCTGGTGGACTTCAGACGCCAAGCCCTGTTCCAGGACAAGAAATTC
AGCCAACTCTGGGTGAGAGGTTCTGGGGATTGTGGTACAGAACACCAAGAGCCCTGTTCCAGGACAAGAAATTC
GTGCTCACTTTCAGCACAGCTACAGCCGAAGAATGTGACTTCGAATGTGTGTTCTGGGTGGAAGCCCACTCA
TTGAGCAGCCCGGGGACTTGGAGCAGTGTCTGGGTGTGAGACCGTCAGGAGAGAAACCAAACTCTGCTCTGCTC
AACCCTTGACTTCTTTCAGTCTGATGGTCTCTCTCGGTGAGGTGGACGCCGTGCAACAAGCACTACTGAGCT
CTCTCTCTCTAGCTGGGCTGTGTCTCTCTGCTCTGCGCTGGCCTGCTCTGTCAACATTTGCCCGCTACTCTGTCTCAGG
GTGCCCCCTCGGTGAGGAGAACTCTCGGACTACACCATCAAGGTGCATGCAACCTGTGCTGTGCGCGCTCTTCT
CTGTGTCACAGAGCTTCTCTGCTCAGCGAGCCGCTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC
ATCTCTGCTGACTCTCTCCCTGCTCAGCTGCTCTTCTGGATGGGCTCGAGGGGTGAACCTCTACCGACTCTGT
GTGGAGGTCTTTTGACCATATGCTCCCTGGCTACCTPACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCATCTTCT
CTGGTGAAGCTGTGGCCCTGTGTGGATGTGGACAACATATGGCCCATCATCTTGGCTGTGATAGGACTCCAGAG
GGCTCTCATCTACCTCTCCATGTGCTGGATCCGGACTCCTCTGTGCTGACTACATCAACCACTTGGGCTCTTCCAGC
CTGTGTCTTCTGTTCATACCTGCTGCTAGCCACCATGGTGTGAGATCTGCGCGCTGGCCCGCCACAGCCAA
AAGTGTGTACATGTGTGACATGTCTGGCCCTCAGCTGTCTCTGGCCCTGGCTGGCTTGTATCTTCTCTCTC
TTTGCTTCTGGCACCTTCTCAGCTGTGTCTCTCTACCTTTTTCAGCATCATCACTGCTTCCAGGCTTCTCTCATC
TTTACTCTGTACTCTGTCCATGCGGCTCGAGGCCCGGGTGGCCCTTCCCTCTGTAAGAGCAACTCAGACAGCGCC
AGGCTCCCATCAGCTCGGGCAGCACTCTGTCAGCCGCATCTAGAGCTCAGCCACCTGCCCATGTATGATGAAG
CAGAGATGCGGCTCTGTGCAACATGCTGTGGCCCCCGAGCCAGGCCCGGCGAGTCAGCCCGAGACT
TTGGAAGGCCAACGACCATGAGAGATGGGCCGTGGCCATGGTGGAGGACTCCCGGGCTGGGCTTTTGAATTG
GCCTTGGGGACTACTCGCTCTCACTCAGCTCCACGGGACTCAGAAGTGGCTGCTGCTGCTAGGGTACTG
TCCCCACATCTGTCCCCAACCGAGCTGGAGGCTTGTCTCTCTTACACCCCTGGGCCCGAGCCCTCATTGTCTGG
GGCCAGGCTTGGATCTTGTAGGCTCTGGCACATCTTAATCTGTGCCCCCTGCTGGGACAGAAATGTGGCTTCA
GTTGCTCTGTCTCTGTGTCACTCTGAGGCACTCTGCATCTCTGTCAATTTTAACTCAGGTGGCACCCAGGG
CGAATGGGGCCCGAGGCGAGCCTTCAGGGCCAGAGCCCTGGCGAGGAGAGGCCCTTTGCCAGGAGCAGCAGC
AGCTCGCTCACTCTGAGCCGAGGCCCCCTCCTCCTCAGCCCCAGCTCTCCTCCTCATCTTCTCCTGGGGTCT
TCTCTCTCTCCAGGGGCTCTTGTCTCTCTGCTTCAAGCTGGGGGTCCCGATTTCAATGCTGTGTCTTTTGGGGA
GTGTTTCCAGAGGCTGCTGTGTCTGTGTAAATGTTTGTCTACTGCACAAGCTCGGGCTGCCCTTGAGCCA
GGCTCGGTACAGGATGCTGTGGGCTGGCTAGGTCTCTGTCTCTGGGCTTGTATGAGCTGCATGCGCCTGT
CTCAGCTGACCAAGCACACGCTCAGAGGGGCCCTCAGCCTCTCTGAAGCCTCTCTGTGGCAGAACTGTGGA
CCATGCACTCCGCTGTGTTTTCATCCCCCACTCCAAGGACTGAGACTGCTCTGTGTGACACTTGCCCTA
GAGCTGACACTCTCTTAAGAGGTTCTCTCAAGCCCCCAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGTGT
TAATTTCTGTGCAAAACACACAGCGGTAGATTGTGCGCTGTTGTAGGTGATAGGACACAGATGACGAGCT
GTCACTCTCTCTGCAACATCTCAGTCTGTGTGTGAGGCTGCGTGAAGCAAGAACTCTGGAGCTACAGGAGCA
GGGAGCCATCATCTTCTCTGGGAATCTTGAAGACTTCTGAGGACTTCTGATCTTGAATGTGAAGAT
GGGAGGATGTTCTTTTACGTACCAATCTTTTGTCTTTTGAATATTAAGAGAAATCATGTTCAATTGTGAGAGA
ATTTTGAAGCTGAGAGAGATCAAGAAAGAAAAATAAAATCAGCTGTGTGATCGCTAGCAAAAAAATAAA
AAAAA

09973268-101501

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFSQQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAHPASRSFPDPGRGLYHFCLYWNRHAGRLHLLYGKRDPELLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSFQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLQL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEQSEIMEYSVLLPRTLFRQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTPVVLTFQHQLQPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRR
TQTSCFCNHLTYFAVLVMSVVEVDVAVHKHYLSLLSYVGCVVSAALACLVTIAAYLCSRVPPLPC
RRKPRDYTIKVMHNNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFFLHFSLLTCLSWMGLE
GYNLYRLVVEVFQTYVPGYLLKLSAMGWGFPIFLVTI VALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSITNLGLFSLVFLFNAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGLFIFIWWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCCTTCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCTGCACTTCTCCTGCTCACCTGCGCTTCTGCTGGATGGGCCCTCGAGGGG
TACAACTCTACCGACTCGTGGTGGAGGTCTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

00075298-101601

Signal sequence:

amino acids 1-14

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTCATTTCCATTTTGGAGA
 AGACTAAAAATGCTGTTTCCAAATGTGGACACTGAAGAGACAAATCTTATCCCTTTTAAACATAATCCCTAAATTTCC
 AAACCTCCTTGGGGCTAGATGGTTTCCCTAAAACCTCTGCCCTGTGATGTCTCCTTGGATGTTCCAAAGAACCATGTG
 ATCTGGGACTGCACAGACAGCAATTTGACAGAAATCTCTGGAGGTATCCACAGAACCCACAGAACTCCACCTC
 ACCATTAACACCATACACAGACATCTCCCGACGCTCCTTTCAAGACCTGGACCATCTGCTAGAGATCGATTTAATCA
 TGCAACTGTGTACCTATTCCACTGGGCTCAAAAAACACATGTGCATCAAGAGGCTGCAGATTAACCCAGAAAGC
 TTTAGTGGACTCAGCTTATTTAAAAATCCCTTTACCTGGATGGAACACGCTACTAGAGATACCCAGGGCTCTCCCG
 CCTAGCTCTACAGCTCTTCAGCTCTGGAGGCCAACACATCTTTTCCATCAGAAAGAGATCTAACAGAACTGGCC
 AACATAGAAATACTCTACTCTGGGCCAAAACCTGTTATTATCGAAATCCCTTGTATTGTTTCATATTCAATAGAGAAA
 GATGCGCTTCTAAACTTGACAAAATTTAAAAGTGTCTCTCCCTGAAAGATAACAATGTCCAGCGCGTCCCTACTGTT
 TTGCCATCTACTTTTAACAGAACTATATCTCTACACACACATGATGCAAAAAATCCAAGAAAGATGATTTTAATAAC
 CTCAACCAATTAACAATTTCTTGACCTAAGTGGAAATGGCCCTCGTTGTATAATGCCCATTTTCTTTGTGGCGCG
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAAATTAAGAGTTTACGCTTA
 CACAGTAATCTCTTTCAGCATGTGCCCCCAAGATGGTTTAAGAACATCAACAACTCCAGGAACTGGATCTGTCC
 CAAAACCTCTTGGCCAAAAGAAATTTGGGATGTCTAAATTTCTGCATTTTCTCCCGACCTCATCCAATTTGGATCTG
 TCTTTCAATTTTGAACCTTCAGGTCTATCGTGCTATGTAATCTATCAACAGCATTTTCTTCACTGAAAAGCCTG
 AAAAATCTCGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATGTCTAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGCTATAGATCTTTCACTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTCTTGCTCAAA
 GCCAGAACTCTCTAGAAAGTTATGAACCCAGGTCCTGGAACAATTACATTTTTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAAACAAAGAGGCTCTTTTCATGTCTGTTAATGAAAGCTGCTACAAGATGGGCGAGCC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTCAGCATCTTTCTTCTCCTCAAAATGCCCTG
 AATCTGTGAGGAATCTCATCTAGCCAAAATCTTAATGGCAGTGAATCCAACTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAACACCGGCTGTATTTACTCCATCAACAGCATTTGAAGAGCTTCACAACTGGAAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTAATTTTCAATCAGAAGGAATTAATCTATGCTAACTTTACCAAGAACCTTAAAGGTT
 CTGCAGAACTGATGATGAACGCAATGACATCTCTTCTCCACAGCAGGACCATGAGAGTGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTATGGAGAGAGGTTGATAACAGATTAATCAATTAATCAAG
 AATCTGCTAAATTAAGAGAAATAGACATCTCTAAATTTCCCTAAGTTCTTGCTTCTGGAGTTTGTGATGTT
 ATGCTCCAAATCTAAAGATCTCTCTTTGGCCAAAATGGGCTCAAACTTTCAAGTGAAGAACTCCAGTGT
 CTAAGAACTCTGGAATCTTGGACCTCAGCCACCACTGACCACTGCTCCCTGAGAGATTTCCACTGCTCC
 AGAAGCTCAGAATCTGATTCTTAAGAAATCAATCAAGAGCTGACAGAAATTTTCAAGATGCTCTTC
 CAGTTGCGATATCTGATCTCAGCTCAAAATAAAATCCAGATGATCCAAAGACACAGCTTCCCAAGAAATGTCCTC
 AACAACTGAAAGATGTTGCTTTTGCATATAATCGGTTTCTGTGACCTGTGATGCTGTGGGTTTGTCTGGTGG
 GTTAACCAATACGAGAGTGACATCTCTTACCTGGCCACAGATGTGACTTGTGTGGGCTGAGAGCACCAAGGSC
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
 TCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGTCACTCTATTTCTGGAGTGTGGGTATATTTACCAT
 TTCTGTAAGGCAAGATAAAGGGGATCAGCGTCTAATATCACCAGACTGTGCTATGATGCTTTTATTGTGTAT
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGGCCAAAATGGAAGACCCAAAGAGAGAAA
 CATTTTAAATTTATGTCTCGAGGAAGGGACTGGTTACAGGGCACCCAGTTCTGGAAGAACTTTCCACAGACATA
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAATTTTAAAGATAGCATTTTAC
 TTGCTCCCATCAGAGGCTCATGGATGAAAGAGTTGATGTGATATCTGTATTTTCTTGAGAAAGCCCTTTCAGAAG
 TCAAGTCTTCCAGCTCGGAAAGAGGCTCTGTGGAGGTTCTGTGCTGTGGCTGGCCACAAACCCCAAGAGCTCC
 CCATATCTTGGCAGTGTCTAAAGAAAGCCCTGGCCACAGACATCATGTGGGCTATGATCAGGTGTTCAAGGAA
 ACGGTCTAGCCCTCTTTGGCAAAACACAACTGCCTAGTTTACCAAGGAGAGGCTGGC

00978298.101501

FIGURE 209

MVFPMTLKRQILILEFNIIISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTNTLTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSILYLDGNQLLEIPQGLPPSLQLLSLEANNIFSRKENLTELANIEILYLQNCYYR
NPCYVVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPPFCAPCKNNSPLQIPVNAFDALTELKVLRLHNSLSLQHVPPRWF
KNINKLQELDLSQNF LAKEIGDAKFLHFLPSLIQLDLSFNFEQVYRASMNLSQAFSSLSKL
KILIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVKNIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLSIQTNGSEFQPLAELRYLDFSNRDLHLH
STAFELHKLLEVLDISSNSHYFQSEGIHMLNFTKNLKVQLKMMNDNDISSSTRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSCLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVWNHTEVTIP
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAEVLAKLEDPREKHFNLCLLE
RDWLPQGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPIFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATAGAACCAACAGAAAACTGGAACACATGTTCTCTTC
 AGTCGTCAATGCTGACCTGCAATTTCTCTGCTAAATATCTGGTTCTCTGAGTTTATGCGCGGAGAAAAATTTTCTA
 GAAGCTATCTCTGTGATGAGAAAAACAAATGACTCAGTTATTTGCAAGTGCAGCAATCGTCTGACTTACGGAAG
 TTCCCAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAATTTCAATCACACATACGAATGAAG
 CATTGTTCAAGGGCTGCAAAATCTCACTAAAAATAAATCTAAACCACACCCCAATGTACAGCACCAGAACGGAAATC
 CGCGTATACAAATCAATGGCTTGAATATCACAGACGGGGCATTCTCTCACTAAAAAACCCTAAGGGAGTTACTGTC
 TTGAAGACACCAAGTTTACCCCAAATACCTCTGGTTTGGCAGAGTCTTTGACACAGCTTAGTCTAAATCAAAACA
 ATATATACAACTAATCAAGAGGGGCATTTCAGACTTATAAATCTTGAATAATCTCTATTGGGCTGGAACTGCT
 ATTTTAAACAAAGTTTGGGAGAAAACTAAACATAGAAGTGGAGTATTTGAACCGCTGACAAATTTTGGAGTTGCTAT
 CACTATCTTTCAATTTCTCTTTCACAGTGCACCCAAACCTGCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA
 CCCAGATCAAACTAATTTAGTGAAGAAGATTTCAAGGATTTGATAAATTTAACTACTAGATTATTAAAGCGGAACCT
 GTCCGAGTGCTCTCAATGCCCAATTTCCATGCGTGCCTTGTGATGGTGGTCTCAATTAATATAGATCTGTTTGG
 CTTTTCAAAACTTGACCCAACTTCGATACCTTAAACCTCTTAGCACTCCCTCAGGAAGATTAAATGTCTGCTGGT
 TTAAAAATATGCTCTCATCTGAAGGTGCTGGATCTTGAATTCACATTTTAGTGGGAGAAATAGTCTCTGCGGCAT
 TTTTAAACGATGCTGCCCGCTTAGAAATACTTGAATTTTAACTATAAAAGGGAGTTATCCACAGCATA
 TTAATATTTCCAGAAATCTTCTAAATCTTTGCTCTAGCGGCATTGCAATTAAGAGGTTATGTTCTCCAGGATA
 TCAGAGAGATGATTTTCCAGCCCTGATGCAGCTTCCAACTTATCGACTATCACTTGGGATTAATTTTATTA
 AGCAAACTCGATTTCAAACTTTCCAAAAATTTCTCCAATCTGGAATTTATTTACTGTGTCAGAAAAACAGAAATACAC
 CGTGGTGAAGAAGTACCCGGCAGGTTATGCAAAATAGTTCTTCTTTCAACGTCATATCCGGAAACGACGCTCAA
 CAGATTTTGGATTTGACCCCACTTGAACCTTTTATCAATTTACCCGCTCTTTAATAAGCCCAATGTGCTGCTT
 ATGAAAAAGCTTAGATTAAAGCTCAACAGTATTTTCTTATTGGGCGAAACCAATTTGAAAATCTTCTGAC
 TTGCTGTTTAAATCTGCTGCAAAATGACAGTCTCAAGTGTTAAGTGAACCTGAAATTTGACCCATGCTCTCATG
 TCAAAATATTTGGATTTGACAAACAAAGACTAGACTAGACTTTGATAAGTGTAGTGTCTTACTGAATTTGCGCATTTGG
 AAGTCTAGATTTCAAGTATAATTTACACTATTTTCAAGATAGCAGGGCTAACACATCTCTAGAATTTTATTCAAA
 AITTCACAACTTCAAAAGTTTAAACTTGAAGCTGAGCCAAACAACTTTATCTTTAACAGATAGTATAACCTGGAAA
 GCAAGTCCCTGGTGAAGATTTAGTTTCAGTGGCAATCGCTTGACATTTTGGGAATGATGATGACAAACAGGATA
 TCTCCATTTTCAAGGCTCTCAAGATCTGACACGCTGGAATTTATCCCTTTAATAGGCTGAAGCACATCCCAATA
 AAGCATTCCTTAATTTGGCCAGCAGTCTCACTGAATACATATAATGATAATATGTTAAAGTTTTTTAACTGGCA
 CATTAATCTCCAGCAGTTTCTCGTCTGAGTTGCTTGACTTACGTTGAAACAACTCTCTTTTAACTGATAGCTT
 TATCTGACTTTACATCTTCCCTTCCGACACTGCTGCTGACTCAATACAGGATTTCCCACTCCCTCTGCGCTTTC
 TTTCTGAAGTCAGTAGTCTGAAGCACTCGATTTAAAGTCCCAATCTGCTAAAAACAACTCAACAACTCCGACTTG
 AAACTAAGACCACCAACAAATTTCTATGTTGGAACTACACCGAAACCCCTTTGAATGCACTGTGACATTTGAG
 ATTTCCGAAGATGGATGGATGAACATCTGGAATGCAAAATTTCCAGACTGGTAGATTTCAATTTGTCGACGCTG
 GGGATCAAAAGAGGGAAGAGTATTTGGAGTCTGGAGCTAAACATCTTGTCTCAGATGTCATGCACTGATATTTAT
 TTTTCTCAGGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCCACATTTGTTTACTGGAGTGT
 GGTTTATATATAATGTTGTTTGAAGTAAAGGCTACAGGTTCTCTTCAAGATCCCAAACTTTCTATGATG
 CTTCATTTCTTATGACACCAAGATGGCTCTGTGTTACTGACTGGGTGATAAATGAGCTGGCGTACCACTGGAAG
 AGAGCCGAGACAAAAAGCTTCTCTTTGCTAGAGGAGAGGGATTGGGACCCGGGATTTGGCCATCATGCAACCT
 TCATGCAAGACATCAACCAAGCAAGAAAAACAGTATTTGTTTAAACAAAAAATGCAAAAAAGCTGGAACCTTTA
 AAACAGCTTTTACTTGGCTTCTGAGAGCTAATGGATGAGACATGGATGTGATTTATTTATCTGCTGGAGC
 CAGTGTTCAGACATCTCTGATTTTGAAGCTACGGCAGCGGATCTGTAAGAGCTCCATCTCCAGTGGCCTGACA
 ACCGGAAGGACAGAGGCTTGTTTTGGCAAACTCTGAGAAATGTGGCTTGAAGTGTGATTTTAAACCAACACA
 ATATGTATGTCGATCCATTAAGCAATACAACTGACGTTAAGTCATGATTTGCGGCCATTAATAAGATGCAAG
 GAATGACATTTCTGATTTAGTTATTTGCTATGTGTAACAAATTTATCCAAATCTAGTGGTTTAAACCAACACA
 TTGCTGCGCCACAGTTTGTGAGGGTCAGGAGTCCAGGCCACGATCACTGGGTCTCTGCTCAGGTTGCTGCTAG
 AGGCTGCAATGAGTGTTCACGAGACATAGGCATCACTGGGTCACTGATTTGTTTCTGAGATTTCA
 ATTCTCTCGGGCTATTTGGCCAAAGGCTATCTCATGTAAGCCATGCGAGCCTCTCCCAACAGGCAAGCTGCTTC
 ATTCAGAGCTAGCAAAAAAGAGGTTGCTAGCAAGATGAAGTCACAACTTTTGTAAATCGAATCAAAAAACACA
 ATCTCATCATCTTTGGCCATTTTCTATTTGTTAGAAGTAAACCAAGTCCACAGGATTCATGGGAGTGACCACC
 TCAGTCCAGGGAACAGCTGACCAAGATGGTGAAGTCTGATTTGCTTGGTGTGCTCATCAACTATTTTCCCT
 TGAAGTGTCTGCTGGGATGGCTGCTATCTGATGATAGATTTGGAATATCAGGAGGCAAGGATCACTGTGGAC
 ATCTTACAGCTGCTTCAACATCACTCTTTTCAATATCTAAGAACTTTGCAATTTAGAGTAAATGGTGTGTTAT
 TTAAGCTGTGTTTATATTTATCATATCTATGGCTACATGGTTATATTTAGTGTGGTTCGGTTCGGTTTAT
 TTGATGCTGCTTTTCAAAATTTTGGTGAACATTTGACTTGAAGTTTATGATGCACTTTAAGACATGATGAT
 ATAGCTTTTAAAGCATCTTTTACTTTCTTACCATTTTAAAGTATGACGCTAAATTCGAGCTTTTGGTCTATA
 TTGTTAATGGCATTTGCTGTAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

0973223.101501

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPYCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLHNPNVQHQNNGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNIITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLLSLFSNLSLHVPPKLPSSLRKLFLSNTQIKYI SEEDFKGLINL
TLDDLSGNCPRCFNAPFPVPCDGGASINIDRFAFQNLTLQRLYNLSSTSLRKINA AWFKNM
PHLKVLDFEFNYLVG EIVS GAFLTMLPRLEILDLSFNYIKGSPQHINISRNFSKLLSLRAL
HLRGVVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNSNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWDDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDLSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDSL
SNLLKTINKSALETKTTTKLSMLELHGPNPECTCDIGDFRRWMD EHLNVKIPRLVDVVICASP
GDQRKSIVSLELTTCVSDVTAVILFFFTFFFITTMVLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGTGCAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGTCTCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTATCCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGTGACATTGCCAGTCA
GATGTGGATGAATGCAGTGTCTAGGAGGGCGGGTGTCCCCAGCGCTGCATCAACCCGCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGACTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCTCTCTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACCTGCCAGCGCCCCAGGCTG
GACTGAGCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCCTTCTCTCTCTCTCTCTCCCC
TTCTCTGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGTCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGAG
GCTGGTGGGCGCTCAGTGGGGGCTGTGCTGCTGACCCCCAGCACAAATAAAATGAAACGTGA
AAAGGGCGGCCGCACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTTATTGCAGCTTATAATGGTTACAAAT

00973298.701501

FIGURE 213

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

0078298 101501

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAAACGGGGGCCCGGGAGGGGAATGGCCCCGAGGGAGAGGAAACCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGCCCTGTCCGGGGATGACTGATTTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCAAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGCTCACGGGACCCCTGTCTCCGAGTCGTTTCG
TGCAGCGTGTGTACAGCCCTTCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGTG
TCCCAGCGCTGCATCAACACCGCCGCGAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGAATGAAGGAAGAGTGTCAGAGGCTGCAGTCCAGGGTGGACCTGTCT
GGAGGAGAAGCTGCAGCTGTGTCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTCTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGA
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCCTCTTCTCCTCCTCCCTTCTCGGGAGGCTCCCCAGACCCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACAGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCCGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

007329 101501
105101 828100

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC
GGGACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG
GCTGGCCCCCTGCCAGGCCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGTCGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGTGGAGGAGAAGCTGCAGCTGGTGTGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCGGCAGCCTCCTGGTGCCTCC
TTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTCTCTGGAGGAGCAGCT
GGGTCTCTGCTCCTGCAAGAAAGACTCGTGA¹CTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCAGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCTTCTCCTGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSADGTLCVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

0075293-10501

FIGURE 219

MSVMVVRKKVTRKWEKLPGRENTFCCDGRVMMARQKGFYLTFLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIPRPPRASHCSICDNCVERFDHHCWPVVGNCVGKRNRYFYFL
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFHTF
LVALNQTINEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLGCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPQEAABAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

00978206 101501

FIGURE 220

AAAACCTGTATTTTTTACAATGCAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTTGGAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

09078208:101501

FIGURE 221

GTGTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTCTTGACACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCCGCAGGGGAGAGCGCCACCTCAGGTGCACCTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA
CAAGTGGTGCCCTGGATCCTCGCGTGGTCTCTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAAACAGACCTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACACACTTTCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCGTCAAGGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGGCTCTGGCTGCTGCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGTGCGGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
GATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCCG
GCACCTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAACGTGAAATAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLNSNTQTQYSIEIQNVVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHNTNASIML
FGPGAVSEVSNGTSTRAGCVWLLPLLVLHLLKF

Signal peptide:

amino acids 1-28

00978298.101501

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

09973293.101501

FIGURE 224

ATGGCTGGTGAACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCGGGGAGCCCTGA
ATCACCGCTTGGCCCGCATCCACCAAGAAACGTGCGCTGCAGAGCTGGGAGCTGGGAGCAACGCTGGGATTCCAG
AAGGGGACAGAGCAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTACGAGCTGCCCTCTCTACTGCTGGCT
GCACCTGCTTCTGGGCTGCTTCTGGGCTCTAGGGTCCAGTACCAAGAGACCCATCCACAGCAGCTGCCCTTACA
GAGGCTTGCATTGAGTGGCTGGAAAAATCTGGAGTCCCTGGACCCGAGGGTGGAGCCCTGTGAGGACCTTTTAC
CAGTTCTCTCTGGGGGCTGGATTCTGGAGGAACCCCTGCCGATGGGGTCTCTGCTGGAAACCTTCAACAGC
CTCTGGGACCAAAACAGGCCATACTGAAGCACCTGCTTGAAGAACCCCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACAGCGCTTCTACCTATCTGCTACAGGTGGAGCGCATTTAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTTGAGAAGATTGGTGGTGGAAACATTACGGGGCCCTGGGACCAAGCAACTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGGCGACTTAAGAGTTCCAACAGC
AATGTTATCCAGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGTCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGATGCTGCTGGGTGGGCGGCCCACTTCCAGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACTCACAGTGCCTCCAGGACAGCGCGCGAC
GAGGAGAGATCTACCAAGATGAGCATTTCGGAGCTCGAGGCTCTGGCGCCCTCCATGGAATGGCTTGAAGTTC
CTGCTCTTCTTGCTGTACCCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGGCTCATCAACCGCAGGAAACCAAGCATCTGAAACAATTACCTGATCTGGAACTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCTCTATGGCACTAAGAAG
TCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACAGGATGAGCGCTTGGCTTTGGCTTTGGGGTCACTCTTC
GTGAAGGCCAGTTTGAACCGCAAGCAAGAAATTCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
GAGGCCCTGGGACAGCTGGTTGGATGGATGAGAAGACCCGCGAGGAGCCAGGAGAAAGCAGATGCCATCTAT
GATATGATTGTTTCCAGACTTTTATCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATCTTTCTTCCAACATGTTGAATTTGTACAACCTCTCTGCAAGGTTATGGCTGACCAAGCTCGCAAG
CCTCCAGCCGAGACAGTGGAGCATGACCCCCAGACAGTGAATGCTTACTCTTCCAACCTAAGAATGAGATC
GTCTTCCCGCTGGCATCTCGCAGGCCCTTCTATGCCCGCAACCAACCCAGGCCCTGAACTCTGGTGGCATC
GGTGTGGTCACTGGCCATGAGTTGACGCTGCTTTGATGACCAAGGGCGGAGTATGACAAAGAGGGAACCTG
CGGCCCTGGTGGCAGAAATGATCTCTGGCAGCTTCCGGAACCAACAGGCCCTGATGGAGGAACAGTACAATCAA
TACAGGTCATGGGAGAGGCTCAACGCGCCGAGACGCTGGGGAGAACTTACTGACAAACGGGGGCTGAAG
GCTGCCCTCAATGCTTCAAAAGCATGGCTGAGAAAGCATGGGAGGAGCACTGCCAGCCGTGGGGCTCACCC
AACCACAGCTCTTCTTCTGGGATTGGCCAGGTGTGGTCTCGGTCCGACACAGAGAGCTCTCACAGGGG
CTGGTGACCGACCCCAAGCCCTGCCCCCTTCCGCTGTGGGCACTCTCTCCAACCTCCCGTACTTCTGCGG
CACTTCCGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTGAACCTGGATCAGGGGA
GAAATGGGCACTGTCAACAGCACTGGGGCAGCTCTCTGACAAAGCTGTTTGTCTCTGGGTGGGAGGAGCAA
ATGCAAGCTGGGCTGGTCTAGTCCCTCCCCCAAGGTGACATGAGTACAGCCCTCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCTCCAGCAGAGCCCCACCATTCATCTGTGACATCTTTCGTGTACCCCT
GCCTGGAAGAGGCTTGGGTGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 225

MNVALQELGAGSNVGFQKGTQQLGSRQTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGWIRRNPLPDGRSRWNTFNSLWDQNA
ILKHLLENTTFNSSEAEQKTQRFYLSCLQVERIEELGAQPLRLDIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTUYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVLTAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLLETLYGTTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEELGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLNYSFAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKENLRPWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFVVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPQGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

FIGURE 227

GGCCGAGCGGGGGTGTCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC
TCCACCATGAACGTGCGCTGCGAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCATGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCCTTACAGAGGCCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTGCGGA
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCACACAGCAATGTTATCCAGGTGGACCAAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCT
CCTTTCTTTCTTCTTTCTTCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTCCTTCTCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCACTGTGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAAGGGTCTGAGGATTGAGGAGAGACTTATGGAGCC
AGCAAAAGTCTTCTGAAGAGATTGCATTGAGCCAGGTCTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAACATAAGAAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC
TTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTTGC CGC
CCTGTTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGTGAAGGCTGCC'TACAATGC'TTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCAAAC'TCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTTCGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCTT
GCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCTCTGT
GTCTTAGGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAAATTAGACACACTCCGGACGCGGCCAAAAAGCAACCCGAGA
GGAGGGGAGGCAAAAACACCCGAAAAACAAAAGAGAGAAAACACCCCAACAACCTGGGGTGG
GGGGAAGAAAGAAAAGAAAAGAAACCCACCCACCCCAAAAAAAGAAAAAAGAAAAA
AAAAAAGAAATTCCTGTGGCGCGCCGCTGGTTCCCGGAAGACTCGCCAGCAGCAGGGGG
TGGGGAGTGCAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGCTG
CTGTTGGTGCAGGGTGCTGTTGCTCGAACCACTGGCTGGCGGGTGCTCCTCAGCCTGTG
CTGCCTGCTACCCCTCGTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCTCGGGCGCCGGTGG
ACAACATGATGTGACAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAATTAAT
TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCACT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTCCAGACTCAACATACACCCAGAACA
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
CGTCAATGAAGGAACCAACGCTCACTCTTACTTGTGTTGGCCACTGGGAAACAGAGCCTTCCA
TTTCTTGGCGACACATCTCCCCACTCAGCAAAAACCAATTTGAAAATGGACAATATTTGGACATT
TATGGAAATTACAAGGGACCAAGGCTGGGGAAATATGAATGCAGTGGGAAAAATGCTGTGTCAAT
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAT
CTGGCACCCGTGACCCCCGGACGCGAGTGGCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT
CCAGCCTTTGAATGGTACAAAGGAGAGAGAAGCTCTTCAATGGCCAAACAGGAATTTATTT
TCAAAAATTTTACGACCAAGATCCATTCTCACTGTTTACCAACGTGACACAGGAGCATTCGGCA
ATTATACCTGTGTGGCTGCCAACAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT
CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCTGCTGGTACCT
TGTGTTGACACTCTCCTCTTCCACGACATATCTACCTGAAGAATGCCATTTCTACAA~~TAAA~~
TTCAAAGCCCAATAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
GGTACAGTTGTTAAAAGCAGCGTGGGATATAATCAGCAGTGTCTGATGGGGATGATCGC
TTCTGTAGAATTGCTCATTATGTAAATACCTTAATTTCTACTCTTTTTTGATTAGCTACATTA
CCTTGTGAAGCAGTACACATTTGCTCTTTTTTAAGACGCTGAAAGCTCTGAAATTAATTTTAG
AGGATATTAATTGTGATTTTCATGTTTGAATCTACAACCTTTCAAAGCAATTCAGTCATGGT
CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATGCAGTGAATATGTGATTTCTTAA
GGCTGCAATAACAGCAATTCAGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAGATG
CATTTTTTTTCTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAAATA
TAACACATATCTAGATTTTTCTGCTTGCATGATATTCAAGTTTCAGGAATGAGCCTTGTAAT
ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTCAGCATGGGTGTCCTTCATAC
AATAATATTTTTCTTCTTGTCTCCAACTAATATAAAATGTTTTGCTAATCTTACAATTTGA
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
TATTGGACTGTAAAAATCTCTCTCGCACTGACAATGGGGTTTGAGAAATTTGCCCCACACT
AACTCAGTCTCTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATGATGATTC
TTTAGTTGTAGCTAAAGTTAGATCCACCGTGGGAAATCATTCCTTTAAATGACAGCA
GTCCACTCAAAGGATTGCTTAGCAATACAGCATCTTTCTCTTCACTAGTCCAAGCCAAAA
TTTTAAGATGATTTGTGAGAAAGGCACAAAGTCTTATCACCTAATATTACAAGAGTTGGTA
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTTAGACAGTGCACCTGGAGGTATGGA
TATGGATATGGACGTTCCAGAGACTATAATGCGAGAAACAGGGTGGTTATGACCGCTACTC
AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA
CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGATTTTATAAAGGTTTTTGG
AGCTGCATCTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTTGACCTGCCA
AGGTAGCTGAAGACCTTTTATAGACAGTTCATCTTTTTTTTAAATTTTTTCTGCCTATTTAA
AGACAAATTATGGGACGTTTGTCAAAAAAAGAAAAAAGAAAAAAGAAAAA

00076298-101501

FIGURE 230

MLLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDFRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIIYDISNDMTVNEGTVNLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFDPVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGT TNASLPL
NPPSTAQYGITGSADVL FSCWYLVLT LSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCCTGGAGAACACCTGGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCGCGGGAGCCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCCTCCAAGGACCCAGGGTGCTTCAGGGAAGCAAG
GAGCCACTGGCACCCCAAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCAAAAGGGGAACTGGAACCTAAGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTATGGGCTCCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGCTGGTTTTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGCCCTCCTGGTGCAGTGGGACACCAGGTGC
CAAGGGTGAGCCTGGCAGTGTCTGGCTCCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAAGGGACACAGGACTTCAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTTCGGCAGTAGTAACCGAGGCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT
ACTCCAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAAGTGTCCGGGCACGAGAGTACCCTGTGGAGCTGCACCAAGAAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGAGGCTGGAGTGCAGCGTCTGACCCCGAAACCTTTTCA
CTTCTCTGCTCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

007625-101501

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGSPSGPQPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLPGSGKDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFFPAKGDQGGPGLQGVPG
PPGAVGHGPAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGLQGGQGRKGESGVPGPA
GVKGEQGSPLAGFPKGAQQAQKQDQGVKGSSGEGQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

00073208 101501

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCAAAAGACGTTTTCTTTGGACCAAAGATCTCTTTG
TGATTCTTGCAACAATCAATGGAATCTTCATGTATTCTGGAGAACACCATTCCTGATTTCT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCCTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

0973206-101501

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1 .

MKLMVLVFTIGLTLLLGVSQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

00076298-101501

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCGCGCTGGTGGTTGGAGGGG
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGGAACTCTCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCGCCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA
 TAAATCCTCCAATGAAGCTACTAACATTACTCCAAGGCATAATATGAAAGCATTTTTGGAT
 GAAATTGAAAGCTGAGAACATTCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAAACAGAACAAAATTTTCAGCTTGCAAAGCAAATTCATCCCACTGGAAGAATTTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTTACCACAAATAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAAC
 ACCTCCTCCAGGATATGAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCTC
 AAGGAATGCCAGAGGGCGATCTAGTGATGTAACTATGCACGAACCTGAAGACTTCTTTAAA
 TTGGAACGGGACATGAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT
 TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCTTGCTGACTACTTTGCTCTGGGGTGAAGTCCATCAGAGCGGTGGAATCTTCTCT
 GGAGGTGGTGTCCAGCTGGGAAATATCCTAAATCTGAACTGGTCAGGAGCCCTTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATGTCAGAGGCTGTTGGTCTTCCAA
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
 TCAGCACCAACCATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTCAATGTTGGACCTGG
 CTTTACTGGAACTTTTCTACACAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA
 CGAGAATTTACAATTGTATAGGTACTCTCAGAGGAGCAGTGGAAACGACAGATATGTCAAT
 CTGGGAGGTCAACGGGACATCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAAGCAGCTGT
 TGTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTCTACTGAGTGGGCA
 GAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGTATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCCTTCCCCAGAGTTTCAAGTGCCATGCCAGGATAAGCAAATTTGGGATCTGG
 AAATGATTTTGGGTTGTTCTTCCAACGACTTGAATTGCTTCAAGCAGGACGCGTATACATA
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGCTATGAAACATAT
 GAGTTGTTGGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTCCG
 AGGAGGGATGTTGTTGAGCTAGCCAATTCATAGTGCTCCTCTTGTATGTGAGATTATG
 CTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGATCATTGATTCACTTTTCTGTCAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTTCAAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTATTATGTCCTATAGGTTTACCAGAC
 AGGCTTTTATAGGCAATGTCTATGCTTCAAGCAGCCAACAAGTATGTCAGGGGAGTC
 ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCCTTCCAAGGCC
 GGGGAGAAGTGAAAGACAGATTTATGTTGACGCTTCAAGTGCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTTGAAGGATTTTATAGAGAATCCGTAATTTGTAATTTGTTGGTATGTCA
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGT
 TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLHETDSAVATARRRWLCAGALVLAGGFLLGLFPGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPPGYENVSDIVPPSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIARYGKVFGRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANERYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTIRYINVIGTLRGAVEPDYV
ILGGHRDSWVPGGIDFPQGAADVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLLQERGAVAYINADSSIEGNYTLRVDCPTPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPSEFGMPRIKSLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVPELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHKNKYAGESFFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713